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(54) Title: NOVEL METHODS OF CONSTRUCTING LIBRARIES OF GENETIC PACKAGES THAT COLLECTIVELY DISPLAY THE MEMBERS OF A DIVERSE FAMILY OF PEPTIDES, POLYPEPTIDES OR PROTEINS

(57) Abstract: Methods useful in constructing libraries that collectively display members of diverse families of peptides, polypeptides or proteins and the libraries produced using those methods. Methods of screening those libraries and the peptides, polypeptides or proteins identified by such screens.

NOVEL METHODS OF CONSTRUCTING LIBRARIES OF GENETIC
PACKAGES THAT COLLECTIVELY DISPLAY THE MEMBERS OF A
DIVERSE FAMILY OF PEPTIDES, POLYPEPTIDES OR PROTEINS

The present invention relates to constructing
5 libraries of genetic packages that display a member of
a diverse family of peptides, polypeptides or proteins
and collectively display at least a portion of the
diversity of the family. In a preferred embodiment,
the displayed polypeptides are human Fabs.

10 More specifically, the invention is directed
to the methods of cleaving single-stranded nucleic
acids at chosen locations, the cleaved nucleic acids
encoding, at least in part, the peptides, polypeptides
or proteins displayed on the genetic packages of the
15 libraries of the invention. In a preferred embodiment,
the genetic packages are filamentous phage or
phagemids.

The present invention further relates to
methods of screening the libraries of genetic packages
20 that display useful peptides, polypeptides and proteins
and to the peptides, polypeptides and proteins
identified by such screening.

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BACKGROUND OF THE INVENTION

It is now common practice in the art to prepare libraries of genetic packages that display a member of a diverse family of peptides, polypeptides or proteins and collectively display at least a portion of the diversity of the family. In many common libraries, the displayed peptides, polypeptides or proteins are related to antibodies. Often, they are Fabs or single chain antibodies.

10 In general, the DNAs that encode members of the families to be displayed must be amplified before they are cloned and used to display the desired member on the surface of a genetic package. Such amplification typically makes use of forward and backward primers.

Such primers can be complementary to sequences native to the DNA to be amplified or complementary to oligonucleotides attached at the 5' or 3' ends of that DNA. Primers that are complementary to sequences native to the DNA to be amplified are disadvantaged in that they bias the members of the families to be displayed. Only those members that contain a sequence in the native DNA that is substantially complementary to the primer will be amplified. Those that do not will be absent from the family. For those members that are amplified, any diversity within the primer region will be suppressed.

For example, in European patent 368,684 B1, the primer that is used is at the 5' end of the V_H region of an antibody gene. It anneals to a sequence region in the native DNA that is said to be "sufficiently well conserved" within a single species. Such primer will bias the members amplified to those

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having this "conserved" region. Any diversity within this region is extinguished.

It is generally accepted that human antibody genes arise through a process that involves a
5 combinatorial selection of V and J or V, D, and J followed by somatic mutations. Although most diversity occurs in the Complementary Determining Regions (CDRs), diversity also occurs in the more conserved Framework Regions (FRs) and at least some of this diversity
10 confers or enhances specific binding to antigens (Ag). As a consequence, libraries should contain as much of the CDR and FR diversity as possible.

To clone the amplified DNAs for display on a genetic package of the peptides, polypeptides or
15 proteins that they encode, the DNAs must be cleaved to produce appropriate ends for ligation to a vector. Such cleavage is generally effected using restriction endonuclease recognition sites carried on the primers. When the primers are at the 5' end of DNA produced from
20 reverse transcription of RNA, such restriction leaves deleterious 5' untranslated regions in the amplified DNA. These regions interfere with expression of the cloned genes and thus the display of the peptides, polypeptides and proteins coded for by them.

25 SUMMARY OF THE INVENTION

It is an object of this invention to provide novel methods for constructing libraries of genetic packages that display a member of a diverse family of peptides, polypeptides or proteins and collectively
30 display at least a portion of the diversity of the family. These methods are not biased toward DNAs that contain native sequences that are complementary to the

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primers used for amplification. They also enable any sequences that may be deleterious to expression to be removed from the amplified DNA before cloning and displaying.

5 It is another object of this invention to provide a method for cleaving single-stranded nucleic acid sequences at a desired location, the method comprising the steps of:

10 (i) contacting the nucleic acid with a single-stranded oligonucleotide, the oligonucleotide being functionally complementary to the nucleic acid in the region in which cleavage is desired and including a sequence that with its complement
15 in the nucleic acid forms a restriction endonuclease recognition site that on restriction results in cleavage of the nucleic acid at the desired location; and

20 (ii) cleaving the nucleic acid solely at the recognition site formed by the complementation of the nucleic acid and the oligonucleotide;

the contacting and the cleaving steps being performed at a temperature sufficient to maintain the nucleic
25 acid in substantially single-stranded form, the oligonucleotide being functionally complementary to the nucleic acid over a large enough region to allow the two strands to associate such that cleavage may occur at the chosen temperature and at the desired location,
30 and the cleavage being carried out using a restriction endonuclease that is active at the chosen temperature.

It is a further object of this invention to provide an alternative method for cleaving single-

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stranded nucleic acid sequences at a desired location,
the method comprising the steps of:

- 5 (i) contacting the nucleic acid with a partially double-stranded oligonucleotide, the single-stranded region of the oligonucleotide being functionally complementary to the nucleic acid in the region in which cleavage is desired, and the double-stranded region of the oligonucleotide having a Type II-S restriction endonuclease recognition site, whose cleavage site is located at a known distance from the recognition site; and
- 10 (ii) cleaving the nucleic acid solely at the cleavage site formed by the complementation of the nucleic acid and the single-stranded region of the oligonucleotide;
- 15

the contacting and the cleaving steps being performed
20 at a temperature sufficient to maintain the nucleic acid in substantially single-stranded form, the oligonucleotide being functionally complementary to the nucleic acid over a large enough region to allow the two strands to associate such that cleavage may occur
25 at the chosen temperature and at the desired location, and the cleavage being carried out using a restriction endonuclease that is active at the chosen temperature.

It is another objective of the present invention to provide a method of capturing DNA
30 molecules that comprise a member of a diverse family of DNAs and collectively comprise at least a portion of the diversity of the family. These DNA molecules in single-stranded form have been cleaved by one of the

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methods of this invention. This method involves ligating the individual single-stranded DNA members of the family to a partially duplex DNA complex. The method comprises the steps of:

5 (i) contacting a single-stranded nucleic acid sequence that has been cleaved with a restriction endonuclease with a partially double-stranded oligonucleotide, the single-stranded region of the oligonucleotide being
10 functionally complementary to the nucleic acid in the region that remains after cleavage, the double-stranded region of the oligonucleotide including any sequences necessary to return the sequences that remain
15 after cleavage into proper reading frame for expression and containing a restriction endonuclease recognition site 5' of those sequences; and

 (ii) cleaving the partially double-stranded oligonucleotide sequence solely at
20 the restriction endonuclease recognition site contained within the double-stranded region of the partially double-stranded oligonucleotide.

25 It is another object of this invention to prepare libraries, that display a diverse family of peptides, polypeptides or proteins and collectively display at least part of the diversity of the family, using the methods and DNAs described above.

30 It is an object of this invention to screen those libraries to identify useful peptides, polypeptides and proteins and to use those substances in human therapy.

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BRIEF DESCRIPTION OF THE DRAWINGS

FIG. 1 is a schematic of various methods that may be employed to amplify VH genes without using primers specific for VH sequences.

5 FIG. 2 is a schematic of various methods that may be employed to amplify VL genes without using VL sequences.

FIG. 3 depicts gel analysis of cleaved kappa DNA from Example 2.

10 FIG. 4 depicts gel analysis of cleaved kappa DNA from Example 2.

FIG. 5 depicts gel analysis of amplified kappa DNA from Example 2.

15 FIG. 6 depicts gel purified amplified kappa DNA from Example 2.

TERMS

In this application, the following terms and abbreviations are used:

20	Sense strand	The upper strand of ds DNA as usually written. In the sense strand, 5'-ATG-3' codes for Met.
25	Antisense strand	The lower strand of ds DNA as usually written. In the antisense strand, 3'-TAC-5' would correspond to a Met codon in the sense strand.

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Forward primer:	A "forward" primer is complementary to a part of the sense strand and primes for synthesis of a new antisense-strand molecule. "Forward primer" and "lower-strand primer" are equivalent.
5	
Backward primer:	A "backward" primer is complementary to a part of the antisense strand and primes for synthesis of a new sense-strand molecule. "Backward primer" and "top-strand primer" are equivalent.
10	
15 Bases:	Bases are specified either by their position in a vector or gene as their position within a gene by codon and base. For example, "89.1" is the first base of codon 89, 89.2 is the second base of codon 89.
20	
Sv	Streptavidin
Ap	Ampicillin
ap ^R	A gene conferring ampicillin resistance.
25	
RE	Restriction endonuclease

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	URE	Universal restriction endonuclease
5	Functionally complementary	Two sequences are sufficiently complementary so as to anneal under the chosen conditions.
	RERS	Restriction endonuclease recognition site
	AA	Amino acid
10	PCR	Polymerization chain reaction
	GLGs	Germline genes
15	Ab	Antibody: an immunoglobulin. The term also covers any protein having a binding domain which is homologous to an immunoglobulin binding domain. A few examples of antibodies within this definition are, <i>inter alia</i> , immunoglobulin isotypes and the Fab, F(ab ¹) ₂ , scfv, Fv, dAb and Fd fragments.
20		
25	Fab	Two chain molecule comprising an Ab light chain and part of a heavy-chain.

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	scFv	A single-chain Ab comprising either VH::linker::VL or VL::linker::VH
	w.t.	Wild type
5	HC	Heavy chain
	LC	Light chain
	VK	A variable domain of a Kappa light chain.
10	VH	A variable domain of a heavy chain.
	VL	A variable domain of a lambda light chain.

In this application, all references referred to are specifically incorporated by reference.

15 DETAILED DESCRIPTION OF THE PREFERRED EMBODIMENTS

The nucleic acid sequences that are useful in the methods of this invention, i.e., those that encode at least in part the individual peptides, polypeptides and proteins displayed on the genetic packages of this
20 invention, may be naturally occurring, synthetic or a combination thereof. They may be mRNA, DNA or cDNA. In the preferred embodiment, the nucleic acids encode antibodies. Most preferably, they encode Fabs.

The nucleic acids useful in this invention
25 may be naturally diverse, synthetic diversity may be

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introduced into those naturally diverse members, or the diversity may be entirely synthetic. For example, synthetic diversity can be introduced into one or more CDRs of antibody genes.

5 Synthetic diversity may be created, for example, through the use of TRIM technology (U.S. 5,869,644). TRIM technology allows control over exactly which amino-acid types are allowed at variegated positions and in what proportions. In TRIM
10 technology, codons to be diversified are synthesized using mixtures of trinucleotides. This allows any set of amino acid types to be included in any proportion.

 Another alternative that may be used to generate diversified DNA is mixed oligonucleotide
15 synthesis. With TRIM technology, one could allow Ala and Trp. With mixed oligonucleotide synthesis, a mixture that included Ala and Trp would also necessarily include Ser and Gly. The amino-acid types allowed at the variegated positions are picked with
20 reference to the structure of antibodies, or other peptides, polypeptides or proteins of the family, the observed diversity in germline genes, the observed somatic mutations frequently observed, and the desired areas and types of variegation.

25 In a preferred embodiment of this invention, the nucleic acid sequences for at least one CDR or other region of the peptides, polypeptides or proteins of the family are cDNAs produced by reverse transcription from mRNA. More preferably, the mRNAs
30 are obtained from peripheral blood cells, bone marrow cells, spleen cells or lymph node cells (such as B-lymphocytes or plasma cells) that express members of naturally diverse sets of related genes. More preferable, the mRNAs encode a diverse family of

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antibodies. Most preferably, the mRNAs are obtained from patients suffering from at least one autoimmune disorder or cancer. Preferably, mRNAs containing a high diversity of autoimmune diseases, such as systemic
5 lupus erythematosus, systemic sclerosis, rheumatoid arthritis, antiphospholipid syndrome and vasculitis are used.

In a preferred embodiment of this invention, the cDNAs are produced from the mRNAs using reverse
10 transcription. In this preferred embodiment, the mRNAs are separated from the cell and degraded using standard methods, such that only the full length (i.e., capped) mRNAs remain. The cap is then removed and reverse transcription used to produce the cDNAs.

15 The reverse transcription of the first (antisense) strand can be done in any manner with any suitable primer. See, e.g., HJ de Haard et al., Journal of Biological Chemistry, 274(26):18218-30 (1999). In the preferred embodiment of this invention
20 where the mRNAs encode antibodies, primers that are complementary to the constant regions of antibody genes may be used. Those primers are useful because they do not generate bias toward subclasses of antibodies. In another embodiment, poly-dT primers may be used (and
25 may be preferred for the heavy-chain genes). Alternatively, sequences complementary to the primer may be attached to the termini of the antisense strand.

In one preferred embodiment of this invention, the reverse transcriptase primer may be
30 biotinylated, thus allowing the cDNA product to be immobilized on streptavidin (Sv) beads. Immobilization can also be effected using a primer labeled at the 5' end with one of a) free amine group, b) thiol, c) carboxylic acid, or d) another group not found in DNA

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that can react to form a strong bond to a known partner on an insoluble medium. If, for example, a free amine (preferably primary amine) is provided at the 5' end of a DNA primer, this amine can be reacted with carboxylic acid groups on a polymer bead using standard amide-forming chemistry. If such preferred immobilization is used during reverse transcription, the top strand RNA is degraded using well-known enzymes, such as a combination of RNaseH and RNaseA, either before or after immobilization.

The nucleic acid sequences useful in the methods of this invention are generally amplified before being used to display the peptides, polypeptides or proteins that they encode. Prior to amplification, the single-stranded DNAs may be cleaved using either of the methods described before. Alternatively, the single-stranded DNAs may be amplified and then cleaved using one of those methods.

Any of the well known methods for amplifying nucleic acid sequences may be used for such amplification. Methods that maximize, and do not bias, diversity are preferred. In a preferred embodiment of this invention where the nucleic acid sequences are derived from antibody genes, the present invention preferably utilizes primers in the constant regions of the heavy and light chain genes and primers to a synthetic sequence that are attached at the 5' end of the sense strand. Priming at such synthetic sequence avoids the use of sequences within the variable regions of the antibody genes. Those variable region priming sites generate bias against V genes that are either of rare subclasses or that have been mutated at the priming sites. This bias is partly due to suppression of diversity within the primer region and partly due to

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lack of priming when many mutations are present in the region complementary to the primer. The methods disclosed in this invention have the advantage of not biasing the population of amplified antibody genes for particular V gene types.

The synthetic sequences may be attached to the 5' end of the DNA strand by various methods well known for ligating DNA sequences together. RT CapExtension is one preferred method.

10 In RT CapExtension (derived from Smart PCR^(TM)), a short overlap (5'-. . .GGG-3' in the upper-strand primer (USP-GGG) complements 3'-CCC....5' in the lower strand) and reverse transcriptases are used so that the reverse complement of the upper-strand primer
15 is attached to the lower strand.

In a preferred embodiment of this invention, the upper strand or lower strand primer may be also biotinylated or labeled at the 5' end with one of a) free amino group, b) thiol, c) carboxylic acid and d)
20 another group not found in DNA that can react to form a strong bond to a known partner as an insoluble medium. These can then be used to immobilize the labeled strand after amplification. The immobilized DNA can be either single or double-stranded.

25 FIG. 1 shows a schematic of the amplification of VH genes. FIG. 1, Panel A shows a primer specific to the poly-dT region of the 3' UTR priming synthesis of the first, lower strand. Primers that bind in the constant region are also suitable. Panel B shows the
30 lower strand extended at its 3' end by three Cs that are not complementary to the mRNA. Panel C shows the result of annealing a synthetic top-strand primer ending in three GGGs that hybridize to the 3' terminal CCCs and extending the reverse transcription extending

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the lower strand by the reverse complement of the synthetic primer sequence. Panel D shows the result of PCR amplification using a 5' biotinylated synthetic top-strand primer that replicates the 5' end of the
5 synthetic primer of panel C and a bottom-strand primer complementary to part of the constant domain. Panel E shows immobilized double-stranded (ds) cDNA obtained by using a 5'-biotinylated top-strand primer.

FIG. 2 shows a similar schematic for
10 amplification of VL genes. FIG. 2, Panel A shows a primer specific to the constant region at or near the 3' end priming synthesis of the first, lower strand. Primers that bind in the poly-dT region are also suitable. Panel B shows the lower strand extended at
15 its 3' end by three Cs that are not complementary to the mRNA. Panel C shows the result of annealing a synthetic top-strand primer ending in three GGGs that hybridize to the 3' terminal CCCs and extending the reverse transcription extending the lower strand by the
20 reverse complement of the synthetic primer sequence. Panel D shows the result of PCR amplification using a 5' biotinylated synthetic top-strand primer that replicates the 5' end of the synthetic primer of panel C and a bottom-strand primer complementary to part of
25 the constant domain. The bottom-strand primer also contains a useful restriction endonuclease site, such as *AscI*. Panel E shows immobilized ds cDNA obtained by using a 5'-biotinylated top-strand primer.

In FIGs. 1 and 2, each V gene consists of a
30 5' untranslated region (UTR) and a secretion signal, followed by the variable region, followed by a constant region, followed by a 3' untranslated region (which typically ends in poly-A). An initial primer for reverse transcription may be complementary to the

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constant region or to the poly A segment of the 3'-UTR. For human heavy-chain genes, a primer of 15 T is preferred. Reverse transcriptases attach several C residues to the 3' end of the newly synthesized DNA.

- 5 RT CapExtension exploits this feature. The reverse transcription reaction is first run with only a lower-strand primer. After about 1 hour, a primer ending in GGG (USP-GGG) and more RTase are added. This causes the lower-strand cDNA to be extended by the reverse
10 complement of the USP-GGG up to the final GGG. Using one primer identical to part of the attached synthetic sequence and a second primer complementary to a region of known sequence at the 3' end of the sense strand, all the V genes are amplified irrespective of their V
15 gene subclass.

- After amplification, the DNAs of this invention are rendered single-stranded. For example, the strands can be separated by using a biotinylated primer, capturing the biotinylated product on
20 streptavidin beads, denaturing the DNA, and washing away the complementary strand. Depending on which end of the captured DNA is wanted, one will choose to immobilize either the upper (sense) strand or the lower (antisense) strand.

- 25 To prepare the single-stranded amplified DNAs for cloning into genetic packages so as to effect display of the peptides, polypeptides or proteins encoded, at least in part, by those DNAs, they must be manipulated to provide ends suitable for cloning and
30 expression. In particular, any 5' untranslated regions and mammalian signal sequences must be removed and replaced, in frame, by a suitable signal sequence that functions in the display host. Additionally, parts of the variable domains (in antibody genes) may be removed

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and replaced by synthetic segments containing synthetic diversity. The diversity of other gene families may likewise be expanded with synthetic diversity.

According to the methods of this invention,
5 there are two ways to manipulate the single-stranded amplified DNAs for cloning. The first method comprises the steps of:

- 10 (i) contacting the nucleic acid with a single-stranded oligonucleotide, the oligonucleotide being functionally complementary to the nucleic acid in the region in which cleavage is desired and including a sequence that with its complement in the nucleic acid forms a restriction
15 endonuclease recognition site that on restriction results in cleavage of the nucleic acid at the desired location; and
- 20 (ii) cleaving the nucleic acid solely at the recognition site formed by the complementation of the nucleic acid and the oligonucleotide;

the contacting and the cleaving steps being performed at a temperature sufficient to maintain the nucleic acid in substantially single-stranded form, the
25 oligonucleotide being functionally complementary to the nucleic acid over a large enough region to allow the two strands to associate such that cleavage may occur at the chosen temperature and at the desired location, and the cleavage being carried out using a restriction
30 endonuclease that is active at the chosen temperature.

In this first method, short oligonucleotides are annealed to the single-stranded DNA so that restriction endonuclease recognition sites formed

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within the now locally double-stranded regions of the DNA can be cleaved. In particular, a recognition site that occurs at the same position in a substantial fraction of the single-stranded DNAs is identical.

5 For antibody genes, this can be done using a catalog of germline sequences. See, e.g.,
"http://www.mrc-cpe.cam.ac.uk/imt-doc/restricted/ok.html." Updates can be obtained from this site under the heading "Amino acid and nucleotide sequence
10 alignments." For other families, similar comparisons exist and may be used to select appropriate regions for cleavage and to maintain diversity.

For example, Table 195 depicts the DNA sequences of the FR3 regions of the 51 known human VH
15 germline genes. In this region, the genes contain restriction endonuclease recognition sites shown in Table 200. Restriction endonucleases that cleave a large fraction of germline genes at the same site are preferred over endonucleases that cut at a variety of
20 sites. Furthermore, it is preferred that there be only one site for the restriction endonucleases within the region to which the short oligonucleotide binds on the single-stranded DNA, e.g., about 10 bases on either side of the restriction endonuclease recognition site.

25 An enzyme that cleaves downstream in FR3 is also more preferable because it captures fewer mutations in the framework. This may be advantageous in some cases. However, it is well known that framework mutations exist and confer and enhance
30 antibody binding. The present invention, by choice of appropriate restriction site, allows all or part of FR3 diversity to be captured. Hence, the method also allows extensive diversity to be captured.

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Finally, in the methods of this invention restriction endonucleases that are active between about 45° and about 75°C are used. Preferably enzymes that are active above 50°C, and more preferably active about 5 55°C, are used. Such temperatures maintain the nucleic acid sequence to be cleaved in substantially single-stranded form.

Enzymes shown in Table 200 that cut many of the heavy chain FR3 germline genes at a single position 10 include: *MaeIII*(24@4), *Tsp45I*(21@4), *HphI*(44@5), *BsaJI*(23@65), *AluI*(23@47), *BlpI*(21@48), *DdeI*(29@58), *BglII*(10@61), *MslI*(44@72), *BsiEI*(23@74), *EaeI*(23@74), *EagI*(23@74), *HaeIII*(25@75), *Bst4CI*(51@86), *HpyCH4III*(51@86), *HinfI*(38@2), *MlyI*(18@2), *PleI*(18@2), 15 *MnlI*(31@67), *HpyCH4V*(21@44), *BsmAI*(16@11), *BpmI*(19@12), *XmnI*(12@30), and *SacI*(11@51). (The notation used means, for example, that *BsmAI* cuts 16 of the FR3 germline genes with a restriction endonuclease recognition site beginning at base 11 of FR3.)

20 For cleavage of human heavy chains in FR3, the preferred restriction endonucleases are: *Bst4CI* (or *TaaI* or *HpyCH4III*), *BlpI*, *HpyCH4V*, and *MslI*. Because ACNGT (the restriction endonuclease recognition site for *Bst4CI*, *TaaI*, and *HpyCH4III*) is found at a 25 consistent site in all the human FR3 germline genes, one of those enzymes is the most preferred for capture of heavy chain CDR3 diversity. *BlpI* and *HpyCH4V* are complementary. *BlpI* cuts most members of the VH1 and VH4 families while *HpyCH4V* cuts most members of the 30 VH3, VH5, VH6, and VH7 families. Neither enzyme cuts VH2s, but this is a very small family, containing only three members. Thus, these enzymes may also be used in preferred embodiments of the methods of this invention.

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The restriction endonucleases *Hpy*CH4III, *Bst*4CI, and *Taa*I all recognize 5'-ACnGT-3' and cut upper strand DNA after n and lower strand DNA before the base complementary to n. This is the most preferred restriction endonuclease recognition site for this method on human heavy chains because it is found in all germline genes. Furthermore, the restriction endonuclease recognition region (ACnGT) matches the second and third bases of a tyrosine codon (tay) and the following cysteine codon (tgy) as shown in Table 206. These codons are highly conserved, especially the cysteine in mature antibody genes.

Table 250 E shows the distinct oligonucleotides of length 22 (except the last one which is of length 20) bases. Table 255 C shows the analysis of 1617 actual heavy chain antibody genes. Of these, 1511 have the site and match one of the candidate oligonucleotides to within 4 mismatches. Eight oligonucleotides account for most of the matches and are given in Table 250 F.1. The 8 oligonucleotides are very similar so that it is likely that satisfactory cleavage will be achieved with only one oligonucleotide (such as H43.77.97.1-02#1) by adjusting temperature, pH, salinity, and the like. One or two oligonucleotides may likewise suffice whenever the germline gene sequences differ very little and especially if they differ very little close to the restriction endonuclease recognition region to be cleaved. Table 255 D shows a repeat analysis of 1617 actual heavy chain antibody genes using only the 8 chosen oligonucleotides. This shows that 1463 of the sequences match at least one of the oligonucleotides to within 4 mismatches and have the site as expected.

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Only 7 sequences have a second *HpyCH4III* restriction endonuclease recognition region in this region.

Another illustration of choosing an appropriate restriction endonuclease recognition site involves cleavage in FR1 of human heavy chains. Cleavage in FR1 allows capture of the entire CDR diversity of the heavy chain.

The germline genes for human heavy chain FR1 are shown in Table 217. Table 220 shows the restriction endonuclease recognition sites found in human germline genes FR1s. The preferred sites are *BsgI* (GTGCAG;39@4), *BsoFI* (GCngc;43@6,11@9,2@3,1@12), *TseI* (Gcwgc;43@6,11@9,2@3,1@12), *MspAI* (CMGckg;46@7,2@1), *PvuII* (CAGctg;46@7,2@1), *AluI* (AGct;48@82@2), *DdeI* (Ctnag;22@52,9@48), *HphI* (tcacc;22@80), *BssKI* (Nccngg;35@39,2@40), *BsaJI* (Ccnngg;32@40,2@41), *BstNI* (CCwgg;33@40), *ScrFI* (CCngg;35@40,2@41), *EcoO109I* (RGgnccy;22@46,11@43), *Sau96I* (Ggncc;23@47,11@44), *AvaII* (Ggwcc;23@47,4@44), *PpuMI* (RGgwccy;22@46,4@43), *BsmFI* (gtccc;20@48), *HinfI* (Gantc;34@16,21@56,21@77), *TfiI* (21@77), *MlyI* (GAGTC;34@16), *MlyI* (gactc;21@56), and *AlwNI* (CAGnnnctg;22@68). The more preferred sites are *MspAI* and *PvuII*. *MspAI* and *PvuII* have 46 sites at 7-12 and 2 at 1-6. To avoid cleavage at both sites, oligonucleotides are used that do not fully cover the site at 1-6. Thus, the DNA will not be cleaved at that site. We have shown that DNA that extends 3, 4, or 5 bases beyond a *PvuII*-site can be cleaved efficiently.

Another illustration of choosing an appropriate restriction endonuclease recognition site involves cleavage in FR1 of human kappa light chains. Table 300 shows the human kappa FR1 germline genes and

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Table 302 shows restriction endonuclease recognition sites that are found in a substantial number of human kappa FR1 germline genes at consistent locations. Of the restriction endonuclease recognition sites listed, 5 *Bsm*AI and *Pfl*FI are the most preferred enzymes. *Bsm*AI sites are found at base 18 in 35 of 40 germline genes. *Pfl*FI sites are found in 35 of 40 germline genes at base 12.

Another example of choosing an appropriate 10 restriction endonuclease recognition site involves cleavage in FR1 of the human lambda light chain. Table 400 shows the 31 known human lambda FR1 germline gene sequences. Table 405 shows restriction endonuclease recognition sites found in human lambda FR1 germline 15 genes. *Hinf*I and *Dde*I are the most preferred restriction endonucleases for cutting human lambda chains in FR1.

After the appropriate site or sites for cleavage are chosen, one or more short oligonucleotides 20 are prepared so as to functionally complement, alone or in combination, the chosen recognition site. The oligonucleotides also include sequences that flank the recognition site in the majority of the amplified genes. This flanking region allows the sequence to 25 anneal to the single-stranded DNA sufficiently to allow cleavage by the restriction endonuclease specific for the site chosen.

The actual length and sequence of the oligonucleotide depends on the recognition site and the 30 conditions to be used for contacting and cleavage. The length must be sufficient so that the oligonucleotide is functionally complementary to the single-stranded DNA over a large enough region to allow the two strands

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to associate such that cleavage may occur at the chosen temperature and solely at the desired location.

Typically, the oligonucleotides of this preferred method of the invention are about 17 to about 5 30 nucleotides in length. Below about 17 bases, annealing is too weak and above 30 bases there can be a loss of specificity. A preferred length is 18 to 24 bases.

Oligonucleotides of this length need not be 10 identical complements of the germline genes. Rather, a few mismatches taken may be tolerated. Preferably, however, no more than 1-3 mismatches are allowed. Such mismatches do not adversely affect annealing of the oligonucleotide to the single-stranded DNA. Hence, the 15 two DNAs are said to be functionally complementary.

The second method to manipulate the amplified single-stranded DNAs of this invention for cloning comprises the steps of:

(i) contacting the nucleic acid with a 20 partially double-stranded oligonucleotide, the single-stranded region of the oligonucleotide being functionally complementary to the nucleic acid in the region in which cleavage is desired, and the 25 double-stranded region of the oligonucleotide having a Type II-S restriction endonuclease recognition site, whose cleavage site is located at a known distance from the recognition site; and

30 (ii) cleaving the nucleic acid solely at the cleavage site formed by the complementation of the nucleic acid and the single-stranded region of the oligonucleotide;

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the contacting and the cleaving steps being performed at a temperature sufficient to maintain the nucleic acid in substantially single-stranded form, the oligonucleotide being functionally complementary to the nucleic acid over a large enough region to allow the two strands to associate such that cleavage may occur at the chosen temperature and at the desired location, and the cleavage being carried out using a restriction endonuclease that is active at the chosen temperature.

10 This second method employs Universal Restriction Endonucleases ("URE"). UREs are partially double-stranded oligonucleotides. The single-stranded portion or overlap of the URE consists of a DNA adapter that is functionally complementary to the sequence to be cleaved in the single-stranded DNA. The double-stranded portion consists of a type II-S restriction endonuclease recognition site.

 The URE method of this invention is specific and precise and can tolerate some (e.g., 1-3) mismatches in the complementary regions, i.e., it is functionally complementary to that region. Further, conditions under which the URE is used can be adjusted so that most of the genes that are amplified can be cut, reducing bias in the library produced from those genes.

 The sequence of the single-stranded DNA adapter or overlap portion of the URE typically consists of about 14-22 bases. However, longer or shorter adapters may be used. The size depends on the ability of the adapter to associate with its functional complement in the single-stranded DNA and the temperature used for contacting the URE and the single-stranded DNA at the temperature used for cleaving the DNA with the type II-S enzyme. The adapter must be

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functionally complementary to the single-stranded DNA over a large enough region to allow the two strands to associate such that the cleavage may occur at the chosen temperature and at the desired location. We
5 prefer single-stranded or overlap portions of 14-17 bases in length, and more preferably 18-20 bases in length.

The site chosen for cleavage using the URE is preferably one that is substantially conserved in the
10 family of amplified DNAs. As compared to the first cleavage method of this invention, these sites do not need to be endonuclease recognition sites. However, like the first method, the sites chosen can be synthetic rather than existing in the native DNA. Such
15 sites may be chosen by references to the sequences of known antibodies or other families of genes. For example, the sequences of many germline genes are reported at <http://www.mrc-cpe.cam.ac.uk/imt-doc/restricted/ok.html>. For example, one preferred
20 site occurs near the end of FR3 -- codon 89 through the second base of codon 93. CDR3 begins at codon 95.

The sequences of 79 human heavy-chain genes are also available at
<http://www.ncbi.nlm.nih.gov/entre2/nucleotide.html>.
25 This site can be used to identify appropriate sequences for URE cleavage according to the methods of this invention. See, e.g., Table 8B.

Most preferably, one or more sequences are identified using these sites or other available
30 sequence information. These sequences together are present in a substantial fraction of the amplified DNAs. For example, multiple sequences could be used to allow for known diversity in germline genes or for frequent somatic mutations. Synthetic degenerate

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sequences could also be used. Preferably, a sequence(s) that occurs in at least 65% of genes examined with no more than 2-3 mismatches is chosen

URE single-stranded adapters or overlaps are
5 then made to be complementary to the chosen regions. Conditions for using the UREs are determined empirically. These conditions should allow cleavage of DNA that contains the functionally complementary sequences with no more than 2 or 3 mismatches but that
10 do not allow cleavage of DNA lacking such sequences.

As described above, the double-stranded portion of the URE includes a Type II-S endonuclease recognition site. Any Type II-S enzyme that is active at a temperature necessary to maintain the single-
15 stranded DNA substantially in that form and to allow the single-stranded DNA adapter portion of the URE to anneal long enough to the single-stranded DNA to permit cleavage at the desired site may be used.

The preferred Type II-S enzymes for use in
20 the URE methods of this invention provide asymmetrical cleavage of the single-stranded DNA. Among these are the enzymes listed in Table 800. The most preferred Type II-S enzyme is FokI.

When the preferred Fok I containing URE is
25 used, several conditions are preferably used to effect cleavage:

- 1) Excess of the URE over target DNA should be present to activate the enzyme. URE present only in equimolar amounts to the target DNA
30 would yield poor cleavage of ssDNA because the amount of active enzyme available would be limiting.
- 2) An activator may be used to activate part of the FokI enzyme to dimerize without causing

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cleavage. Examples of appropriate activators are shown in Table 510.

- 3) The cleavage reaction is performed at a temperature between 45°-75°C, preferably
5 above 50°C and most preferably above 55°C.

The UREs used in the prior art contained a 14-base single-stranded segment, a 10-base stem (containing a FokI site), followed by the palindrome of the 10-base stem. While such UREs may be used in the
10 methods of this invention, the preferred UREs of this invention also include a segment of three to eight bases (a loop) between the FokI restriction endonuclease recognition site containing segments. In the preferred embodiment, the stem (containing the FokI
15 site) and its palindrome are also longer than 10 bases. Preferably, they are 10-14 bases in length. Examples of these "lollipop" URE adapters are shown in Table 5.

One example of using a URE to cleave an single-stranded DNA involves the FR3 region of human
20 heavy chain. Table 508 shows an analysis of 840 full-length mature human heavy chains with the URE recognition sequences shown. The vast majority (718/840=0.85) will be recognized with 2 or fewer mismatches using five UREs (VHS881-1.1, VHS881-1.2, VHS881-2.1, VHS881-4.1, and VHS881-9.1). Each has a
25 20-base adaptor sequence to complement the germline gene, a ten-base stem segment containing a FokI site, a five base loop, and the reverse complement of the first stem segment. Annealing those adapters, alone or in
30 combination, to single-stranded antisense heavy chain DNA and treating with FokI in the presence of, e.g., the activator FOKIact, will lead to cleavage of the antisense strand at the position indicated.

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Another example of using a URE(s) to cleave a single-stranded DNA involves the FR1 region of the human Kappa light chains. Table 512 shows an analysis of 182 full-length human kappa chains for matching by the four 19-base probe sequences shown. Ninety-six percent of the sequences match one of the probes with 2 or fewer mismatches. The URE adapters shown in Table 512 are for cleavage of the sense strand of kappa chains. Thus, the adaptor sequences are the reverse complement of the germline gene sequences. The URE consists of a ten-base stem, a five base loop, the reverse complement of the stem and the complementation sequence. The loop shown here is TTGTT, but other sequences could be used. Its function is to interrupt the palindrome of the stems so that formation of a lollypop monomer is favored over dimerization. Table 512 also shows where the sense strand is cleaved.

Another example of using a URE to cleave a single-stranded DNA involves the human lambda light chain. Table 515 shows analysis of 128 human lambda light chains for matching the four 19-base probes shown. With three or fewer mismatches, 88 of 128 (69%) of the chains match one of the probes. Table 515 also shows URE adapters corresponding to these probes. Annealing these adapters to upper-strand ssDNA of lambda chains and treatment with *FokI* in the presence of FOKIact at a temperature at or above 45°C will lead to specific and precise cleavage of the chains.

The conditions under which the short oligonucleotide sequences of the first method and the UREs of the second method are contacted with the single-stranded DNAs may be empirically determined. The conditions must be such that the single-stranded DNA remains in substantially single-stranded form.

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More particularly, the conditions must be such that the single-stranded DNA does not form loops that may interfere with its association with the oligonucleotide sequence or the URE or that may themselves provide
5 sites for cleavage by the chosen restriction endonuclease.

The effectiveness and specificity of short oligonucleotides (first method) and UREs (second method) can be adjusted by controlling the
10 concentrations of the URE adapters/oligonucleotides and substrate DNA, the temperature, the pH, the concentration of metal ions, the ionic strength, the concentration of chaotropes (such as urea and formamide), the concentration of the restriction
15 endonuclease(e.g., *FokI*), and the time of the digestion. These conditions can be optimized with synthetic oligonucleotides having: 1) target germline gene sequences, 2) mutated target gene sequences, or 3) somewhat related non-target sequences. The goal is to
20 cleave most of the target sequences and minimal amounts of non-targets.

In the preferred embodiment of this invention, the single-stranded DNA is maintained in substantially that form using a temperature between
25 45°C to 75°C. More preferably, a temperature between 50°C and 60°C, most preferably between 55°C and 60°C, is used. These temperatures are employed both when contacting the DNA with the oligonucleotide or URE and when cleaving the DNA using the methods of this
30 invention.

The two cleavage methods of this invention have several advantages. The first method allows the individual members of the family of single-stranded DNAs to be cleaved solely at one substantially

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conserved endonuclease recognition site. The method also does not require an endonuclease recognition site to be built in to the reverse transcription or amplification primers. Any native or synthetic site in
5 the family can be used.

The second method has both of these advantages. In addition, the URE method allows the single-stranded DNAs to be cleaved at positions where no endonuclease recognition site naturally occurs or
10 has been synthetically constructed.

Most importantly, both cleavage methods permit the use of 5' and 3' primers so as to maximize diversity and then cleavage to remove unwanted or deleterious sequences before cloning and display.

15 After cleavage of the amplified DNAs using one of the methods of this invention, the DNA is prepared for cloning. This is done by using a partially duplexed synthetic DNA adapter, whose terminal sequence is based on the specific cleavage
20 site at which the amplified DNA has been cleaved.

The synthetic DNA is designed such that when it is ligated to the cleaved single-stranded DNA, it allows that DNA to be expressed in the correct reading frame so as to display the desired peptide, polypeptide
25 or protein on the surface of the genetic package.

Preferably, the double-stranded portion of the adapter comprises the sequence of several codons that encode the amino acid sequence characteristic of the family of peptides, polypeptides or proteins up to the cleavage
30 site. For human heavy chains, the amino acids of the 3-23 framework are preferably used to provide the sequences required for expression of the cleaved DNA.

Preferably, the double-stranded portion of the adapter is about 12 to 100 bases in length. More

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preferably, about 20 to 100 bases are used. The double-standard region of the adapter also preferably contains at least one endonuclease recognition site useful for cloning the DNA into a suitable display
5 vector (or a recipient vector used to archive the diversity). This endonuclease restriction site may be native to the germline gene sequences used to extend the DNA sequence. It may be also constructed using degenerate sequences to the native germline gene
10 sequences. Or, it may be wholly synthetic.

The single-stranded portion of the adapter is complementary to the region of the cleavage in the single-stranded DNA. The overlap can be from about 2 bases up to about 15 bases. The longer the overlap,
15 the more efficient the ligation is likely to be. A preferred length for the overlap is 7 to 10. This allows some mismatches in the region so that diversity in this region may be captured.

The single-stranded region or overlap of the partially duplexed adapter is advantageous because it
20 allows DNA cleaved at the chosen site, but not other fragments to be captured. Such fragments would contaminate the library with genes encoding sequences that will not fold into proper antibodies and are
25 likely to be non-specifically sticky.

One illustration of the use of a partially duplexed adaptor in the methods of this invention involves ligating such adaptor to a human FR3 region that has been cleaved, as described above, at 5'-ACnGT-
30 3' using HpyCH4III, Bst4CI or TaaI.

Table 250 F.2 shows the bottom strand of the double-stranded portion of the adaptor for ligation to the cleaved bottom-strand DNA. Since the HpyCH4III-Site is so far to the right (as shown in Table 206), a

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sequence that includes the *Afl*III-site as well as the *Xba*I site can be added. This bottom strand portion of the partially-duplexed adaptor, H43.XAExt, incorporates both *Xba*I and *Afl*III-sites. The top strand
5 of the double-stranded portion of the adaptor has neither site (due to planned mismatches in the segments opposite the *Xba*I and *Afl*III-Sites of H43.XAExt), but will anneal very tightly to H43.XAExt. H43AExt contains only the *Afl*III-site and is to be used with the
10 top strands H43.ABr1 and H43.ABr2 (which have intentional alterations to destroy the *Afl*III-site).

After ligation, the desired, captured DNA can be PCR amplified again, if desired, using in the preferred embodiment a primer to the downstream
15 constant region of the antibody gene and a primer to part of the double-standard region of the adapter. The primers may also carry restriction endonuclease sites for use in cloning the amplified DNA.

After ligation, and perhaps amplification, of
20 the partially double-stranded adapter to the single-stranded amplified DNA, the composite DNA is cleaved at chosen 5' and 3' endonuclease recognition sites.

The cleavage sites useful for cloning depend on the phage or phagemid into which the cassette will
25 be inserted and the available sites in the antibody genes. Table 1 provides restriction endonuclease data for 75 human light chains. Table 2 shows corresponding data for 79 human heavy chains. In each Table, the endonucleases are ordered by increasing frequency of
30 cutting. In these Tables, Nch is the number of chains cut by the enzyme and Ns is the number of sites (some chains have more than one site).

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From this analysis, *SfiI*, *NotI*, *AflIII*, *ApaI*, and *AscI* are very suitable. *SfiI* and *NotI* are preferably used in pCES1 to insert the heavy-chain display segment. *ApaI* and *AscI* are preferably used in
5 pCES1 to insert the light-chain display segment.

BstEII-sites occur in 97% of germ-line JH genes. In rearranged V genes, only 54/79 (68%) of heavy-chain genes contain a *BstEII*-Site and 7/61 of these contain two sites. Thus, 47/79 (59%) contain a
10 single *BstEII*-Site. An alternative to using *BstEII* is to cleave via UREs at the end of JH and ligate to a synthetic oligonucleotide that encodes part of CH1.

One example of preparing a family of DNA sequences using the methods of this invention involves
15 capturing human CDR 3 diversity. As described above, mRNAs from various autoimmune patients is reverse transcribed into lower strand cDNA. After the top strand RNA is degraded, the lower strand is immobilized and a short oligonucleotide used to cleave the cDNA
20 upstream of CDR3. A partially duplexed synthetic DNA adapter is then annealed to the DNA and the DNA is amplified using a primer to the adapter and a primer to the constant region (after FR4). The DNA is then cleaved using *BstEII* (in FR4) and a restriction
25 endonuclease appropriate to the partially double-stranded adapter (e.g., *Xba I* and *AflIII* (in FR3)). The DNA is then ligated into a synthetic VH skeleton such as 3-23.

One example of preparing a single-stranded
30 DNA that was cleaved using the URE method involves the human Kappa chain. The cleavage site in the sense strand of this chain is depicted in Table 512. The

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oligonucleotide kapextURE is annealed to the oligonucleotides (kaBR01UR, kaBR02UR, kaBR03UR, and kaBR04UR) to form a partially duplex DNA. This DNA is then ligated to the cleaved soluble kappa chains. The
5 ligation product is then amplified using primers kapextUREPCR and CKForeAsc (which inserts a AscI site after the end of C kappa). This product is then cleaved with ApaLI and AscI and ligated to similarly cut recipient vector.

10 Another example involves the cleavage illustrated in Table 515. After cleavage, an extender (ON_LamEx133) and four bridge oligonucleotides (ON_LamB1-133, ON_LamB2-133, ON_LamB3-133, and ON_LamB4-133) are annealed to form a partially duplex DNA. That DNA is
15 ligated to the cleaved lambda-chain sense strands. After ligation, the DNA is amplified with ON_Lam133PCR and a forward primer specific to the lambda constant domain, such as CL2ForeAsc or CL7ForeAsc (Table 130).

In human heavy chains, one can cleave almost
20 all genes in FR4 (downstream, i.e. toward the 3' end of the sense strand, of CDR3) at a BstEII-Site that occurs at a constant position in a very large fraction of human heavy-chain V genes. One then needs a site in FR3, if only CDR3 diversity is to be captured, in FR2,
25 if CDR2 and CDR3 diversity is wanted, or in FR1, if all the CDR diversity is wanted. These sites are preferably inserted as part of the partially double-stranded adaptor.

The preferred process of this invention is to
30 provide recipient vectors having sites that allow cloning of either light or heavy chains. Such vectors are well known and widely used in the art. A preferred phage display vector in accordance with this invention

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is phage MALIA3. This displays in gene III. The sequence of the phage MALIA3 is shown in Table 120A (annotated) and Table 120B (condensed).

The DNA encoding the selected regions of the
5 light or heavy chains can be transferred to the vectors using endonucleases that cut either light or heavy chains only very rarely. For example, light chains may be captured with *Apa*LI and *Asc*I. Heavy-chain genes are preferably cloned into a recipient vector having *Sfi*I,
10 *Nco*I, *Xba*I, *Afl*III, *Bst*EII, *Apa*I, and *Not*I sites. The light chains are preferably moved into the library as *Apa*LI-*Asc*I fragments. The heavy chains are preferably moved into the library as *Sfi*I-*Not*I fragments.

Most preferably, the display is had on the
15 surface of a derivative of M13 phage. The most preferred vector contains all the genes of M13, an antibiotic resistance gene, and the display cassette. The preferred vector is provided with restriction sites that allow introduction and excision of members of the
20 diverse family of genes, as cassettes. The preferred vector is stable against rearrangement under the growth conditions used to amplify phage.

In another embodiment of this invention, the diversity captured by the methods of the present
25 invention may be displayed in a phagemid vector (e.g., pCES1) that displays the peptide, polypeptide or protein on the III protein. Such vectors may also be used to store the diversity for subsequent display using other vectors or phage.

30 In another embodiment, the mode of display may be through a short linker to three possible anchor domains. One anchor domain being the final portion of M13 III ("IIIstump"), a second anchor being the full

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length III mature protein, and the third being the M13 VIII mature protein.

The IIIstump fragment contains enough of M13 III to assemble into phage but not the domains involved in mediating infectivity. Because the w.t. III and VIII proteins are present, the phage is unlikely to delete the antibody genes and phage that do delete these segments receive only a very small growth advantage. For each of the anchor domains, the DNA encodes the w.t. AA sequence, but differs from the w.t. DNA sequence to a very high extent. This will greatly reduce the potential for homologous recombination between the display anchor and the w.t. gene that is also present.

Most preferably, the present invention uses a complete phage carrying an antibiotic-resistance gene (such as an ampicillin-resistance gene) and the display cassette. Because the w.t. *iii* and *viii* genes are present, the w.t. proteins are also present. The display cassette is transcribed from a regulatable promoter (e.g., P_{LacZ}). Use of a regulatable promoter allows control of the ratio of the fusion display gene to the corresponding w.t. coat protein. This ratio determines the average number of copies of the display fusion per phage (or phagemid) particle.

Another aspect of the invention is a method of displaying peptides, polypeptides or proteins (and particularly Fabs) on filamentous phage. In the most preferred embodiment this method displays FABs and comprises:

- a) obtaining a cassette capturing a diversity of segments of DNA encoding the elements:

$P_{reg}::RBS1::SS1::VL::CL::stop::RBS2::SS2::VH::CH1::$

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linker::anchor::stop::,

where P_{reg} is a regulatable promoter, RBS1 is a first ribosome binding site, SS1 is a signal sequence
5 operable in the host strain, VL is a member of a diverse set of light-chain variable regions, CL is a light-chain constant region, stop is one or more stop codons, RBS2 is a second ribosome binding site, SS2 is a second signal sequence operable in the host strain,
10 VH is a member of a diverse set of heavy-chain variable regions, CH1 is an antibody heavy-chain first constant domain, linker is a sequence of amino acids of one to about 50 residues, anchor is a protein that will assemble into the filamentous phage particle and stop
15 is a second example of one or more stop codons; and
b) positioning that cassette within the phage genome to maximize the viability of the phage and to minimize the potential for deletion of the cassette or parts thereof.

20

The DNA encoding the anchor protein in the above preferred cassette should be designed to encode the same (or a closely related) amino acid sequence as is found in one of the coat proteins of the phage, but
25 with a distinct DNA sequence. This is to prevent unwanted homologous recombination with the w.t. gene. In addition, the cassette should be placed in the intergenic region. The positioning and orientation of the display cassette can influence the behavior of the
30 phage.

In one embodiment of the invention, a transcription terminator may be placed after the second stop of the display cassette above (e.g., Trp). This will reduce interaction between the display cassette

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and other genes in the phage antibody display vector (PADV).

In another embodiment of the methods of this invention, the phage or phagemid can display proteins
5 other than Fab, by replacing the Fab portions indicated above, with other protein genes.

Various hosts can be used for growth of the display phage or phagemids of this invention. Such hosts are well known in the art. In the preferred
10 embodiment, where Fabs are being displayed, the preferred host should grow at 30°C and be RecA⁻ (to reduce unwanted genetic recombination) and EndA⁻ (to make recovery of RF DNA easier). It is also preferred that the host strain be easily transformed by
15 electroporation.

XL1-Blue MRF' satisfies most of these preferences, but does not grow well at 30°C. XL1-Blue MRF' does grow slowly at 38°C and thus is an acceptable host. TG-1 is also an acceptable host although it is
20 RecA⁺ and EndA⁺. XL1-Blue MRF' is more preferred for the intermediate host used to accumulate diversity prior to final construction of the library.

After display, the libraries of this invention may be screened using well known and
25 conventionally used techniques. The selected peptides, polypeptides or proteins may then be used to treat disease. Generally, the peptides, polypeptides or proteins for use in therapy or in pharmaceutical compositions are produced by isolating the DNA encoding
30 the desired peptide, polypeptide or protein from the member of the library selected. That DNA is then used in conventional methods to produce the peptide, polypeptides or protein it encodes in appropriate host cells, preferably mammalian host cells, e.g., CHO

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cells. After isolation, the peptide, polypeptide or protein is used alone or with pharmaceutically acceptable compositions in therapy to treat disease.

EXAMPLES

5 Example 1: Capturing kappa chains with BsmAI:

A repertoire of human-kappa chain mRNAs was prepared by treating total or poly(A+) RNA isolated from a collection of patients having various autoimmune diseases with calf intestinal phosphatase to remove the
10 5'-phosphate from all molecules that have them, such as ribosomal RNA, fragmented mRNA, tRNA and genomic DNA. Full length mRNA (containing a protective 7-methyl cap structure) is unaffected. The RNA is then treated with tobacco acid pyrophosphatase to remove the cap
15 structure from full length mRNAs leaving a 5'-monophosphate group.

Full length mRNA's were modified with an adaptor at the 5' end and then reversed transcribed and amplified using the GeneRACE™ method and kit
20 (Invitrogen). A 5' biotinylated primer complementary to the adaptor and a 3' primer complementary to a portion of the construct region were used.

Approximately 2 micrograms (ug) of human kappa-chain (Igkappa) gene RACE material with biotin
25 attached to 5'-end of upper strand was immobilized on 200 microliters (μL) of Seradyn magnetic beads. The lower strand was removed by washing the DNA with 2 aliquots 200 μL of 0.1 M NaOH (pH 13) for 3 minutes for the first aliquot followed by 30 seconds for the second
30 aliquot. The beads were neutralized with 200 μL of 10 mM Tris (pH 7.5) 100 mM NaCl. The short oligonucleotides shown in Table 525 were added in 40

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fold molar excess in 100 μ L of NEB buffer 2 (50 mM NaCl, 10 mM Tris-HCl, 10 mM MgCl₂, 1 mM dithiothreitol pH 7.9) to the dry beads. The mixture was incubated at 95°C for 5 minutes then cooled down to 55°C over 30
5 minutes. Excess oligonucleotide was washed away with 2 washes of NEB buffer 3 (100 mM NaCl, 50 mM Tris-HCl, 10 mM MgCl₂, 1 mM dithiothreitol pH 7.9). Ten units of BsmAI (NEB) were added in NEB buffer 3 and incubated for 1 h at 55°C. The cleaved downstream DNA was
10 collected and purified over a Qiagen PCR purification column (FIGs. 3 and 4).

A partially double-stranded adaptor was prepared using the oligonucleotide shown in Table 525. The adaptor was added to the single-stranded DNA in 100
15 fold molar excess along with 1000 units of T4 DNA ligase (NEB) and incubated overnight at 16°C. The excess oligonucleotide was removed with a Qiagen PCR purification column. The ligated material was amplified by PCR using the primers kapPCRT1 and kapfor
20 shown in Table 525 for 10 cycles with the program shown in Table 530.

The soluble PCR product was run on a gel and showed a band of approximately 700 n, as expected (FIGs. 5 and 6). The DNA was cleaved with enzymes
25 ApaLI and AscI, gel purified, and ligated to similarly cleaved vector pCES1. The presence of the correct size insert was checked by PCR in several clones as shown in FIG. 15.

Table 500 shows the DNA sequence of a kappa
30 light chain captured by this procedure. Table 501 shows a second sequence captured by this procedure. The closest bridge sequence was complementary to the sequence 5'-agccacc-3', but the sequence captured reads

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5'-Tgccacc-3', showing that some mismatch in the overlapped region is tolerated.

Example 2: Construction of Synthetic CDR1 and CDR2 Diversity in V-3-23 VH Framework

5 A synthetic Complementary Determinant Region (CDR) 1 and 2 diversity was constructed in the 3-23 VH framework in a two step process: first, a vector containing the 3-23 VH framework was constructed, and then, a synthetic CDR 1 and 2 was assembled and cloned
10 into this vector.

For construction of the V3-23 framework, 8 oligos and two PCR primers (long oligonucleotides: TOPFR1A, BOTFR1B, BOTFR2, BOTFR3, F06, BOTFR4, ON-vgC1, and ON-vgC2 and primers: SFPRMET and BOTPCRPRIM, shown in
15 Table 600) that overlap were designed based on the Genbank sequence of V323 VH. The design incorporated at least one useful restriction site in each framework region, as shown in Table 600. In Table 600, the segments that were synthesized are shown as bold, the
20 overlapping regions are underscored, and the PCR priming regions at each end are underscored. A mixture of these 8 oligos was combined at a final concentration of 2.5uM in a 20ul Polymerase Chain Reaction (PCR) reaction. The PCR mixture contained 200uM dNTPs, 2.5mM
25 MgCl₂, 0.02U *Pfu Turbo*TM DNA Polymerase, 1U Qiagen HotStart Taq DNA Polymerase, and 1X Qiagen PCR buffer. The PCR program consisted of 10 cycles of 94°C for 30s, 55°C for 30s, and 72°C for 30s. The assembled V3-23 DNA sequence was then amplified, using 2.5ul of a 10-
30 fold dilution from the initial PCR in 100ul PCR reaction. The PCR reaction contained 200uM dNTPs, 2.5mM MgCl₂, 0.02U *Pfu Turbo*TM DNA Polymerase, 1U Qiagen

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HotStart Taq DNA Polymerase, 1X Qiagen PCR Buffer and 2 outside primers (SFPRMET and BOTPCRPRIM) at a concentration of 1uM. The PCR program consisted of 23 cycles at 94°C for 30s, 55°C for 30s, and 72°C for 60s.

5 The V3-23 VH DNA sequence was digested and cloned into pCES1 (phagemid vector) using the *Sfi*I and *Bst*EII restriction endonuclease sites (All restriction enzymes mentioned herein were supplied by New England BioLabs, Beverly, MA and used as per manufacturer's

10 instructions).

Stuffer sequences (shown in Table 610 and Table 620) were introduced into pCES1 to replace CDR1/CDR2 sequences (900 bases between *Bsp*EI and *Xba*I RE sites) and CDR3 sequences (358 bases between *Afl*II and *Bst*EII), prior to cloning the CDR1/CDR2 diversity.

15 The new vector is pCES5 and its sequence is given in Table 620. Having stuffers in place of the CDRs avoids the risk that a parental sequence would be over-represented in the library. The CDR1-2 stuffer

20 contains restriction sites for *Bgl*II, *Bsu*36I, *Bcl*I, *Xcm*I, *Mlu*I, *Pvu*II, *Hpa*I, and *Hinc*II, the underscored sites being unique within the vector pCES5. The stuffer that replaces CDR3 contains the unique restriction endonuclease site *Rsr*II. The stuffer

25 sequences are fragments from the penicillase gene of *E. coli*.

For the construction of the CDR1 and CDR2 diversity, 4 overlapping oligonucleotides (ON-vgC1, ON_Br12, ON_CD2Xba, and ON-vgC2, shown in Table 600

30 and Table 630) encoding CDR1/2, plus flanking regions, were designed. A mix of these 4 oligos was combined at a final concentration of 2.5uM in a 40ul PCR reaction. Two of the 4 oligos contained variegated sequences

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positioned at the CDR1 and the CDR2. The PCR mixture contained 200uM dNTPs, 2.5U Pwo DNA Polymerase (Roche), and 1X Pwo PCR buffer with 2mM MgSO₄. The PCR program consisted of 10 cycles at 94°C for 30s, 60°C for 30s, and 72°C for 60s. This assembled CDR1/2 DNA sequence was amplified, using 2.5ul of the mixture in 100ul PCR reaction. The PCR reaction contained 200uM dNTPs, 2.5U Pwo DNA Polymerase, 1X Pwo PCR Buffer with 2mM MgSO₄ and 2 outside primers at a concentration of 1uM. The PCR program consisted of 10 cycles at 94°C for 30s, 60°C for 30s, and 72°C for 60s. These variegated sequences were digested and cloned into the V3-23 framework in place of the CDR1/2 stuffer.

We obtained approximately 7×10^7 independent transformants. Into this diversity, we can clone CDR3 diversity either from donor populations or from synthetic DNA.

It will be understood that the foregoing is only illustrative of the principles of this invention and that various modifications can be made by those skilled in the art without departing from the scope of and spirit of the invention.

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We claim:

1. A method for cleaving single-stranded nucleic acid sequences at a desired location, the method comprising the steps of:

- 5 (i) contacting the nucleic acid with a single-stranded oligonucleotide, the oligonucleotide being functionally complementary to the nucleic acid in the region in which cleavage is desired and
10 including a sequence that with its complement in the nucleic acid forms a restriction endonuclease recognition site that on restriction results in cleavage of the nucleic acid at the desired location; and
15 (ii) cleaving the nucleic acid solely at the recognition site formed by the complementation of the nucleic acid and the oligonucleotide;

the contacting and the cleaving steps being performed
20 at a temperature sufficient to maintain the nucleic acid in substantially single-stranded form, the oligonucleotide being functionally complementary to the nucleic acid over a large enough region to allow the two strands to associate such that cleavage may occur
25 at the chosen temperature and at the desired location, and the cleavage being carried out using a restriction endonuclease that is active at the chosen temperature.

2. A method for cleaving single-stranded nucleic acid sequences at a desired location, the
30 method comprising the steps of:

- (i) contacting the nucleic acid with a partially double-stranded oligonucleotide,

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- the single-stranded region of the oligonucleotide being functionally complementary to the nucleic acid in the region in which cleavage is desired, and the double-stranded region of the oligonucleotide having a Type II-S restriction endonuclease recognition site, whose cleavage site is located at a known distance from the recognition site; and
- (ii) cleaving the nucleic acid solely at the Type II-S cleavage site formed by the complementation of the nucleic acid and the single-stranded region of the oligonucleotide;
- the contacting and the cleaving steps being performed at a temperature sufficient to maintain the nucleic acid in substantially single-stranded form, the oligonucleotide being functionally complementary to the nucleic acid over a large enough region to allow the two strands to associate such that cleavage may occur at the chosen temperature and at the desired location, and the cleavage being carried out using a restriction endonuclease that is active at the chosen temperature.

3. In a method for displaying a member of a diverse family of peptides, polypeptides or proteins on the surface of a genetic package and collectively displaying at least a part of the diversity of the family, the improvement being characterized in that the displayed at least a part of peptide, polypeptide or protein is encoded at least in part by a nucleic acid that has been cleaved at a desired location by a method comprising the steps of:

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- (i) contacting the nucleic acid with a single-stranded oligonucleotide, the oligonucleotide being functionally complementary to the nucleic acid in the region in which cleavage is desired and including a sequence that with its complement in the nucleic acid forms a restriction endonuclease recognition site that on restriction results in cleavage of the nucleic acid at the desired location; and
- (ii) cleaving the nucleic acid solely at the recognition site formed by the complementation of the nucleic acid and the oligonucleotide;
- the contacting and the cleaving steps being performed at a temperature sufficient to maintain the nucleic acid in substantially single-stranded form, the oligonucleotide being functionally complementary to the nucleic acid over a large enough region to allow the two strands to associate such that cleavage may occur at the chosen temperature and at the desired location, and the cleavage being carried out using a restriction endonuclease that is active at the chosen temperature.

4. In a method for displaying a member of a diverse family of peptides, polypeptides or proteins on the surface of a genetic package and collectively displaying at least a part of the diversity of the family, the improvement being characterized in that the displayed peptide, polypeptide or protein is encoded by a DNA sequence comprising a nucleic acid that has been cleaved at a desired location by

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- (i) contacting the nucleic acid with a partially double-stranded oligonucleotide, the single-stranded region of the oligonucleotide being functionally complementary to the nucleic acid in the region in which cleavage is desired, and the double-stranded region of the oligonucleotide having a Type II-S restriction endonuclease recognition site, whose cleavage site is located at a known distance from the recognition site; and
- (ii) cleaving the nucleic acid solely at the Type II-S cleavage site formed by the complementation of the nucleic acid and the single-stranded region of the oligonucleotide;

the contacting and the cleaving steps being performed at a temperature sufficient to maintain the nucleic acid in substantially single-stranded form, the oligonucleotide being functionally complementary to the nucleic acid over a large enough region to allow the two strands to associate such that cleavage may occur at the chosen temperature and at the desired location, and the cleavage being carried out using a restriction endonuclease that is active at the chosen temperature.

5. A method for displaying a member of a diverse family of peptides, polypeptides or proteins on the surface of a genetic package and collectively displaying at least a part of the diversity of the family, the method comprising the steps of:

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(i) preparing a collection of nucleic acids that code at least in part for members of the diverse family;

(ii) rendering the nucleic acids single-
5 stranded;

(iii) cleaving the single-stranded nucleic acids at a desired location by a method comprising the steps of:

(a) contacting the nucleic acid with a
10 single-stranded oligonucleotide, the oligonucleotide being functionally complementary to the nucleic acid in the region in which cleavage is desired and including a sequence that with its complement
15 in the nucleic acid forms a restriction endonuclease recognition site that on restriction results in cleavage of the nucleic acid at the desired location; and

(b) cleaving the nucleic acid solely at
20 the recognition site formed by the complementation of the nucleic acid and the oligonucleotide;

the contacting and the cleaving steps being performed at a temperature sufficient to maintain
25 the nucleic acid in substantially single-stranded form, the oligonucleotide being functionally complementary to the nucleic acid over a large enough region to allow the two strands to associate such that cleavage may occur at the
30 chosen temperature and at the desired location, and the cleavage being carried out using a restriction endonuclease that is active at the chosen temperature; and

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(iv) displaying a member of the family of peptides, polypeptides or proteins coded, at least in part, by the cleaved nucleic acids on the surface of the genetic package and collectively displaying at
5 least a portion of the diversity of the family.

6. A method for displaying a member of a diverse family of peptides, polypeptides or proteins on the surface of a genetic package and collectively displaying at least a portion of the diversity of the
10 family, the method comprising the steps of:

(i) preparing a collection of nucleic acids that code, at least in part, for members of the diverse family;

(ii) rendering the nucleic acids single-
15 stranded;

(iii) cleaving the single-stranded nucleic acids at a desired location by a method comprising the steps of:

(a) contacting the nucleic acid with a
20 partially double-stranded oligonucleotide, the single-stranded region of the oligonucleotide being functionally complementary to the nucleic acid in the region in which cleavage is desired, and the
25 double-stranded region of the oligonucleotide having a Type II-S restriction endonuclease recognition site, whose cleavage site is located at a known distance from the recognition site; and

(b) cleaving the nucleic acid solely at
30 the Type II-S cleavage site formed by the complementation of the nucleic acid and the

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single-stranded region of the
oligonucleotide;

the contacting and the cleaving steps being
performed at a temperature sufficient to maintain
5 the nucleic acid in substantially single-stranded
form, the oligonucleotide being functionally
complementary to the nucleic acid over a large
enough region to allow the two strands to
associate such that cleavage may occur at the
10 chosen temperature and at the desired location,
and the restriction being carried out using a
cleavage endonuclease that is active at the chosen
temperature; and

(iv) displaying a member of the family of
15 peptides, polypeptides or proteins coded, at least in
part, by the cleaved nucleic acids on the surface of
the genetic package and collectively displaying at
least a portion of the diversity of the family.

7. A library comprising a collection of
20 genetic packages that display a member of a diverse
family of peptides, polypeptides or proteins and
collectively display at least a portion of the
diversity of the family, the library being produced
using the methods of claims 3, 4, 5 or 6.

25 8. A library comprising a collection of
genetic packages that display a member of a diverse
family of peptides, polypeptides or proteins and that
collectively display at least a portion of the family,
the displayed peptides, polypeptides or proteins being
30 encoded by DNA sequences comprising at least in part
sequences produced by cleaving single-stranded nucleic

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acid sequences at a desired location by a method comprising the steps of:

- 5 (i) contacting the nucleic acid with a single-stranded oligonucleotide, the oligonucleotide being functionally complementary to the nucleic acid in the region in which cleavage is desired and including a sequence that with its complement in the nucleic acid forms a restriction
10 endonuclease recognition site that on restriction results in cleavage of the nucleic acid at the desired location; and
- 15 (ii) cleaving the nucleic acid solely at the recognition site formed by the complementation of the nucleic acid and the oligonucleotide;

the contacting and the cleaving steps being performed at a temperature sufficient to maintain the nucleic acid in substantially single-stranded form, the
20 oligonucleotide being functionally complementary to the nucleic acid over a large enough region to allow the two strands to associate such that cleavage may occur at the chosen temperature and at the desired location, and the cleavage being carried out using a restriction
25 endonuclease that is active at the chosen temperature.

9. A library comprising a collection of genetic packages that display a member of a diverse family of peptides, polypeptides or proteins and that collectively display at least a portion of the
30 diversity of the family of the displayed peptides, polypeptides or proteins being encoded by DNA sequences comprising at least in part sequences produced by

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cleaving single-stranded nucleic acid sequences at a desired location by a method comprising the steps of:

- 5 (i) contacting the nucleic acid with a partially double-stranded oligonucleotide, the single-stranded region of the oligonucleotide being functionally complementary to the nucleic acid in the region in which cleavage is desired, and the double-stranded region of the oligonucleotide having a Type II S restriction endonuclease recognition site, whose cleavage site is located at a known distance from the recognition site where the cleavage of the nucleic acid is desired; and
- 10 (ii) cleaving the nucleic acid solely at the Type II-S cleavage site formed by the complementation of the nucleic acid and the single-stranded region of the oligonucleotide;
- 15 the contacting and the cleaving steps being performed at a temperature sufficient to maintain the nucleic acid in substantially single-stranded form, the oligonucleotide being functionally complementary to the nucleic acid over a large enough region to allow the
- 20 two strands to associate such that cleavage may occur at the chosen temperature and at the desired location, and the cleavage being carried out using a restriction endonuclease that is active at the chosen temperature.

10. The methods according to any one of
30 claims 1 to 9, wherein the nucleic acids encode at least a portion of an immunoglobulin.

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11. The methods according to claim 10,
wherein the immunoglobulin comprises a Fab or single
chain Fv.

12. The methods according to claim 10 or 11,
5 wherein the immunoglobulin comprises at least portion of
a heavy chain.

13. The methods according to claim 12,
wherein at least a portion of the heavy chain is human.

14. The methods according to claim 10 or 11,
10 wherein the immunoglobulin comprises at least a portion
of FR1.

15. The methods according to claim 14,
wherein at least a portion of the FR1 is human.

16. The methods according to claim 10 or 11,
15 wherein the immunoglobulin comprises at least a portion
of a light chain.

17. The methods according to claim 16,
wherein at least a portion of the light chain is human.

20 18. The methods according to any one of
claims 1 to 9, wherein the nucleic acid sequences are
at least in part derived from patients suffering from
at least one autoimmune disease and/or cancer.

19. The methods according to claim 18,
25 wherein the autoimmune disease is selected from the
group comprising lupus, erythematosus, systemic

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sclerosis, rheumatoid arthritis, antiphospholipid syndrome or vasculitis.

20. The methods according to claim 18,
wherein the nucleic acids are at least in part isolated
5 from the group comprising peripheral blood cells, bone
marrow cells spleen cells or lymph node cells.

21. The methods according to claim 5 or 6
further comprising an nucleic acid amplification step
between steps (i) and (ii), between steps (ii) and
10 (iii) or between steps (iii) and (iv).

22. The methods according to claim 21,
wherein the amplification step uses geneRACE™.

23. The methods according to any one of
claims 1 to 9, wherein the temperature is between 45°C
15 and 75°C.

24. The methods according to claim 23,
wherein the temperature is between 50°C and 60°C.

25. The methods according to claim 24,
wherein the temperature is between 55°C and 60°C.

20 26. The methods according to claim 1, 3, 5
or 8, wherein the length of the single-stranded
oligonucleotide is between 17 and 30 bases.

27. The methods according to claim 26,
wherein the length of the single-stranded
25 oligonucleotide is between 18 and 24 bases.

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28. The methods according to claim 1, 3, 5 or 8, wherein the restriction endonuclease is selected from the group comprising *MaeIII*, *Tsp45I*, *HphI*, *BsaJI*, *AluI*, *BlpI*, *DdeI*, *BglII*, *MslI*, *BsiEI*, *EaeI*, *EagI*,
5 *HaeIII*, *Bst4CI*, *HpyCH4III*, *HinfI*, *MlyI*, *PleI*, *MnlI*, *HpyCH4V*, *BsmAI*, *BpmI*, *XmnI*, or *SacI*.

29. The methods according to claim 28, wherein the restriction endonuclease is selected from the group comprising *Bst4CI*, *TaaI*, *HpyCH4III*, *BlpI*,
10 *HpyCH4V* or *MslI*.

30. The methods according to claim 2, 4, 6 or 9, wherein the length of the single-stranded region of the partially double-stranded oligonucleotide is between 14 and 22 bases.

15 31. The methods according to claim 30, wherein the length of the single-stranded region of the partially double-stranded oligonucleotide is between 14 and 17 bases.

32. The methods according to claim 31,
20 wherein the length of the single-stranded region of the oligonucleotide is between 18 and 20 bases.

33. The methods according to claim 2, 4, 6 or 9, wherein the length of the double-stranded region of the partially double-stranded oligonucleotide is
25 between 10 and 14 base pairs formed by a stem and its palindrome.

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34. The methods according to claim 33 wherein, the partially double-stranded oligonucleotide comprises a loop of 3 to 8 bases between the stem and the palindrome.

5 35. The methods according to claim 2, 4, 6 or 9, wherein the Type II-S restriction endonuclease is selected from the group comprising AarICAC, AceIII, Bbr7I, BbvI, BbvII, Bce83I, BceAI, BceFI, BciVI, BfiI, BinI, BscAI, BseRI, BsmFI, BspMI, EciI, Eco57I, FauI, 10 FokI, GsuI, HgaI, HphI, MboII, MlyI, MmeI, MnlI, PleI, RleAI, SfaNI, SspD5I, Sth132I, StsI, TaqII, Tth111II, or UbaPI.

36. The methods according to claim 35, wherein the Type II-S restriction endonuclease is *FokI*.

15 37. A method for preparing single-stranded nucleic acids for cloning into an vector, the method comprising the steps of:

(i) contacting a single-stranded nucleic acid sequence that has been cleaved with a 20 restriction endonuclease with a partially double-stranded oligonucleotide, the single-stranded region of the oligonucleotide being functionally complementary to the nucleic acid in the region that remains after 25 cleavage, the double-stranded region of the oligonucleotide including any sequences necessary to return the sequences that remain after cleavage into proper and original reading frame for expression and containing a 30 restriction endonuclease recognition site 5' of those sequences; and

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5 (ii) cleaving the partially double-stranded oligonucleotide sequence solely at the restriction endonuclease recognition site contained within the double-stranded region of the partially double-stranded oligonucleotide.

38. The method according to claim 37, wherein the length of the single-stranded portion of the partially double-stranded oligonucleotide is
10 between 2 and 15 bases.

39. The method according to claim 38, wherein the length of the single-stranded portion of the partially double-stranded oligonucleotide is between 7 and 10 bases.

15 40. The method according to claim 37, wherein the length of the double-stranded portion of the partially double-stranded oligonucleotide is between 12 and 100 base pairs.

20 41. The method according to claim 40, wherein the length of the double-stranded portion of the partially double-stranded oligonucleotide is between 20 and 100 base pairs.

AMPLIFY VH GENES WITHOUT
USING VH SEQUENCES

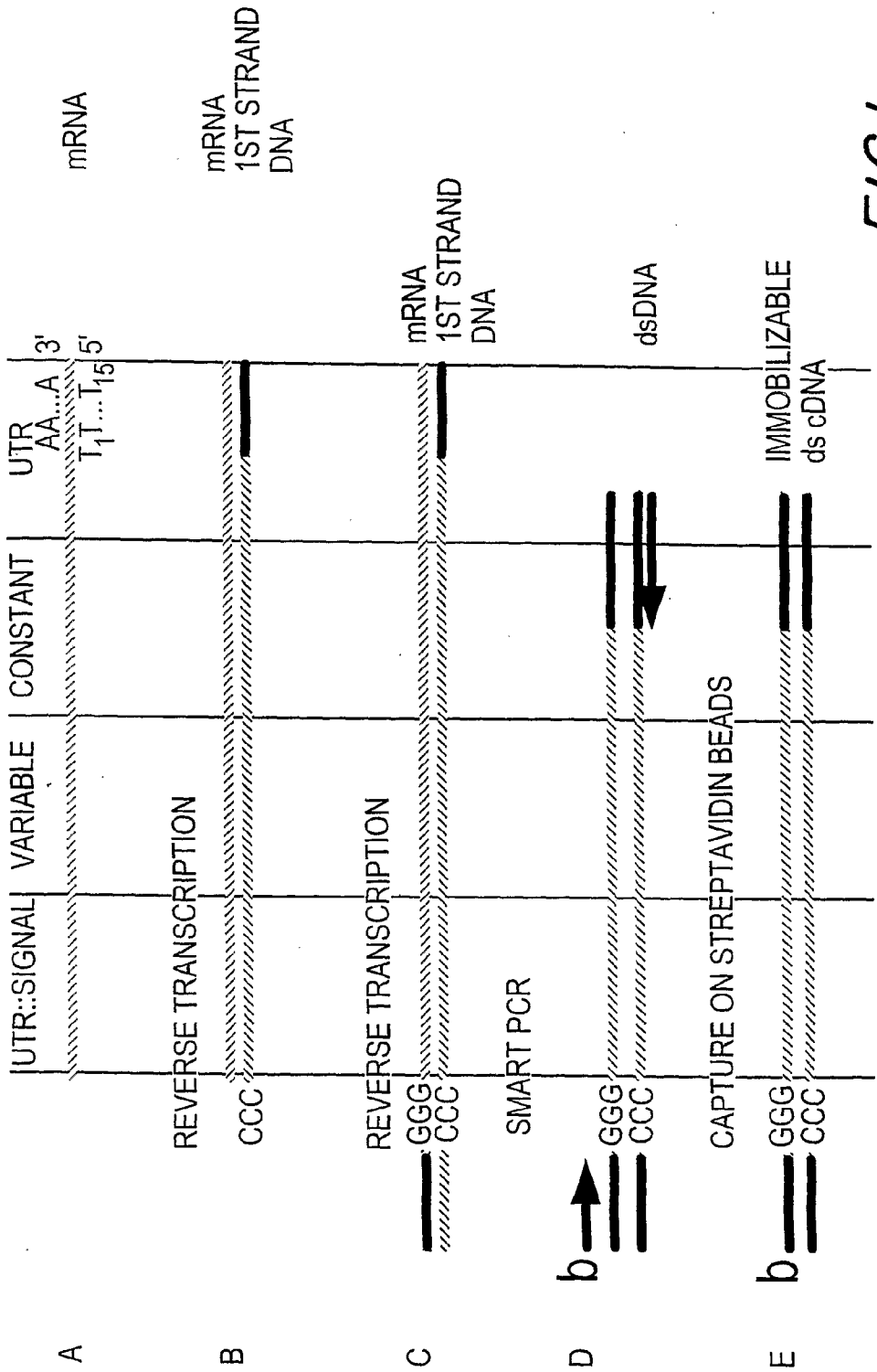


FIG.1

AMPLIFY VL GENES WITHOUT
USING VL SEQUENCES

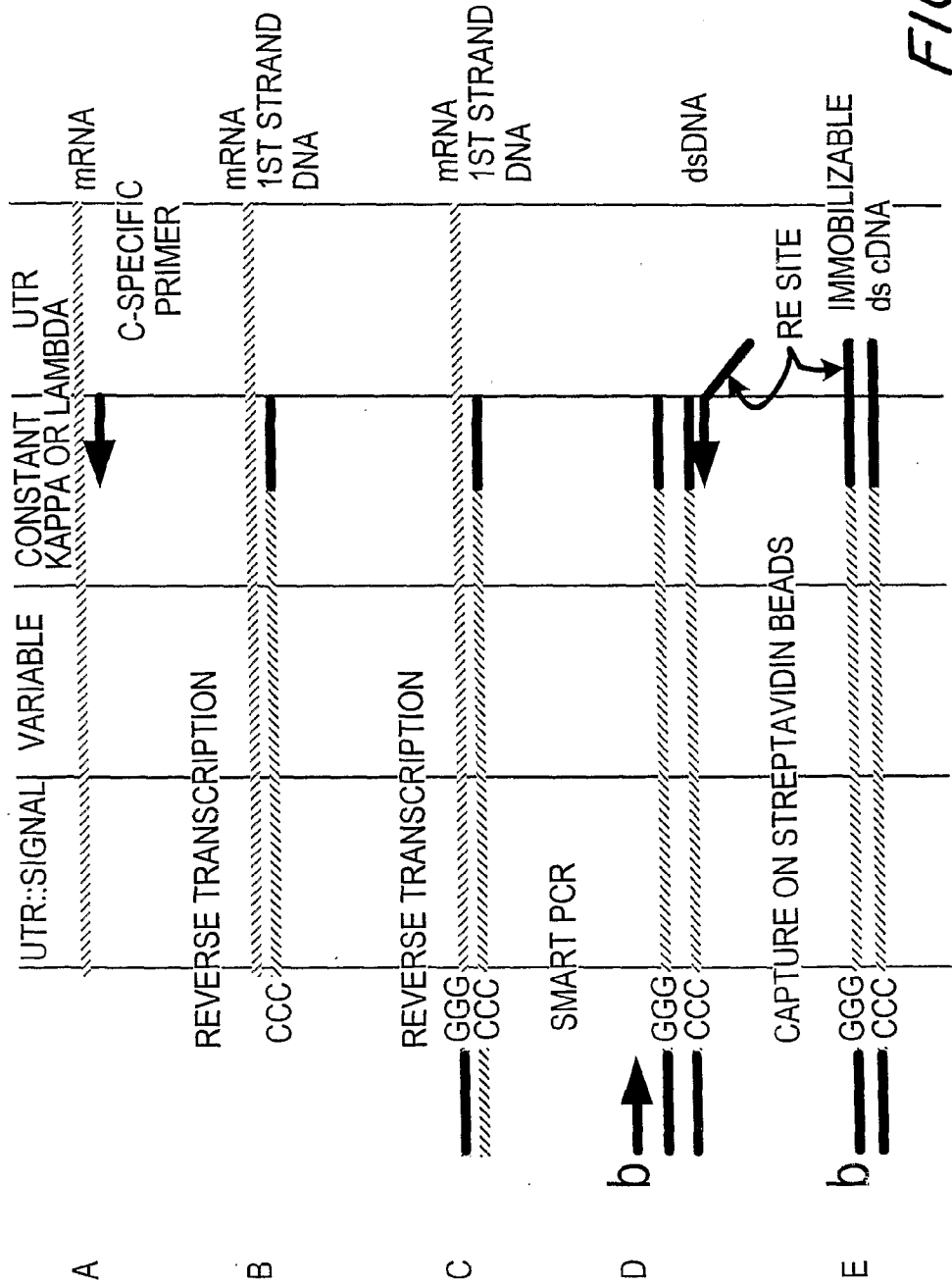
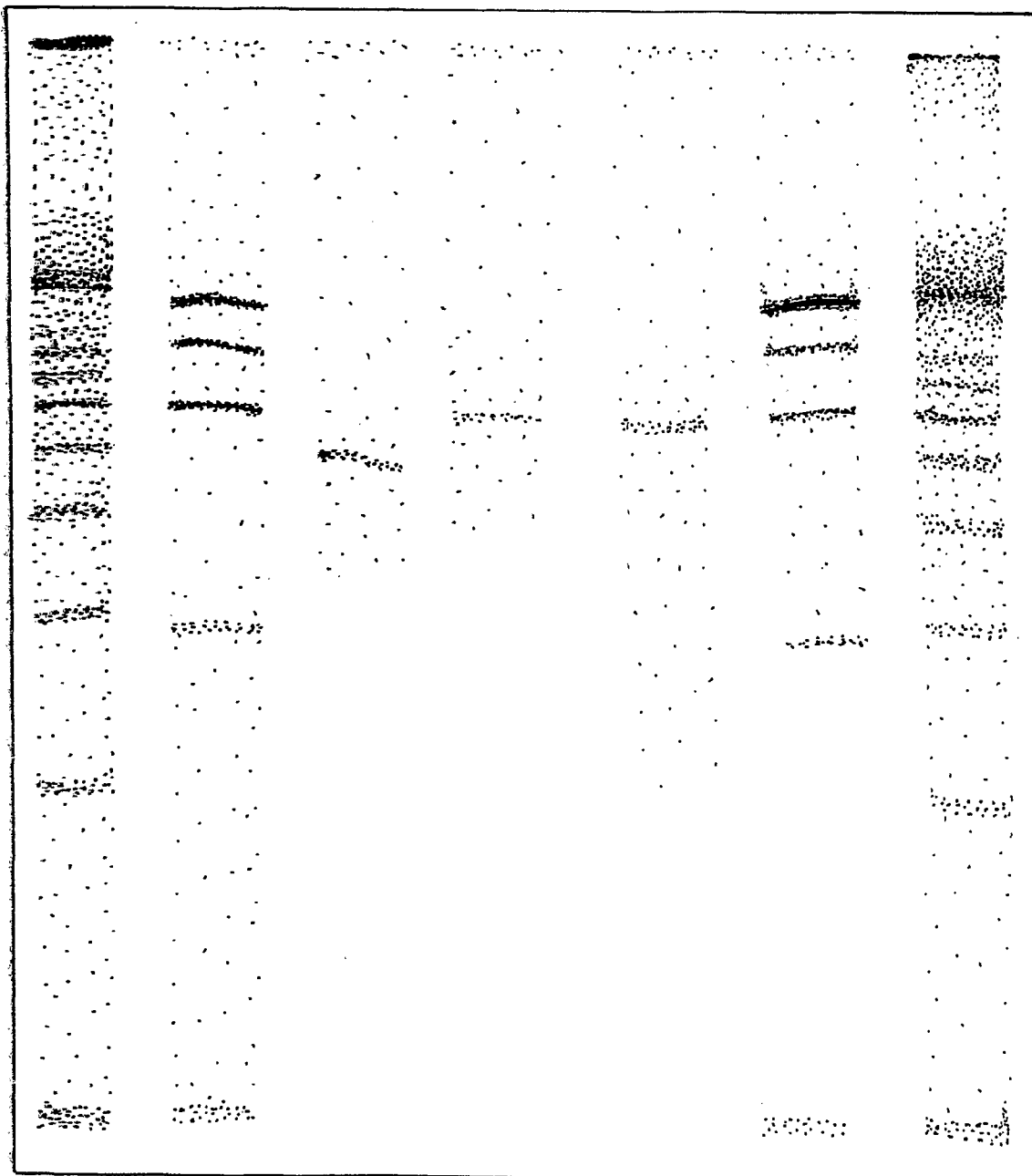
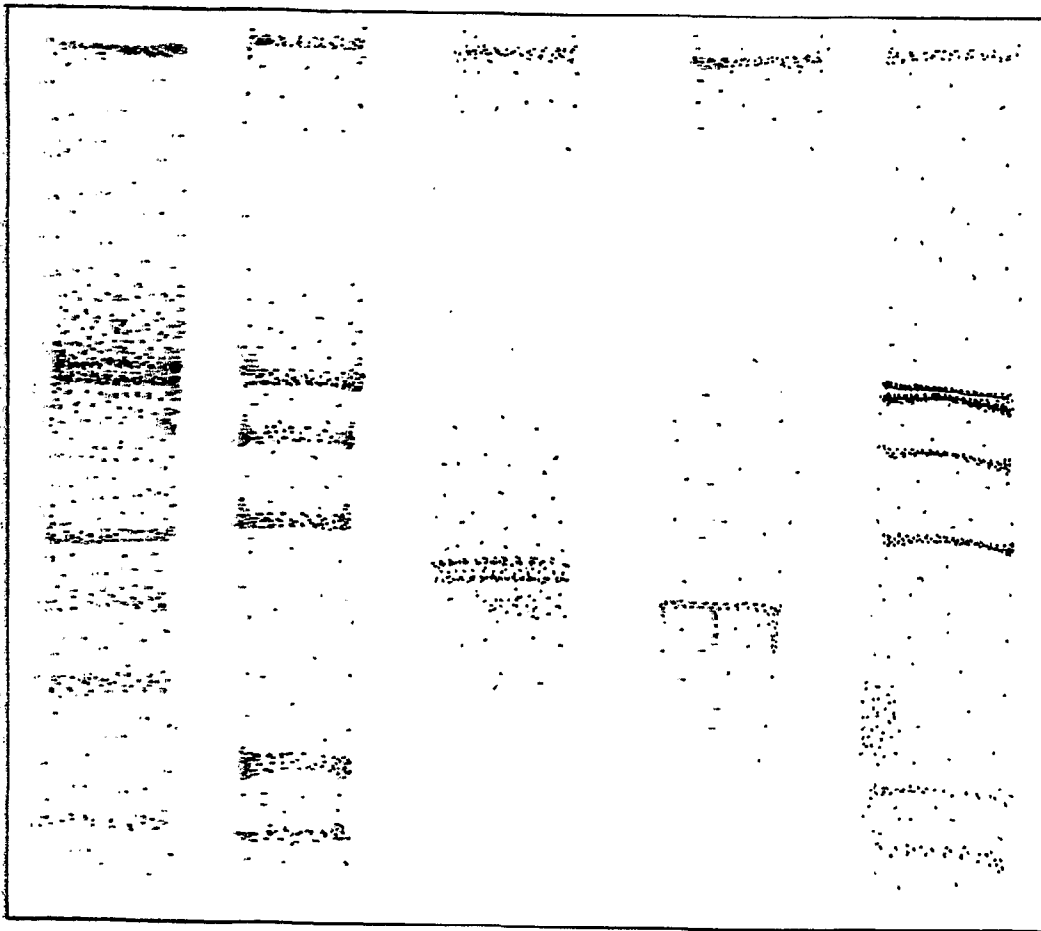
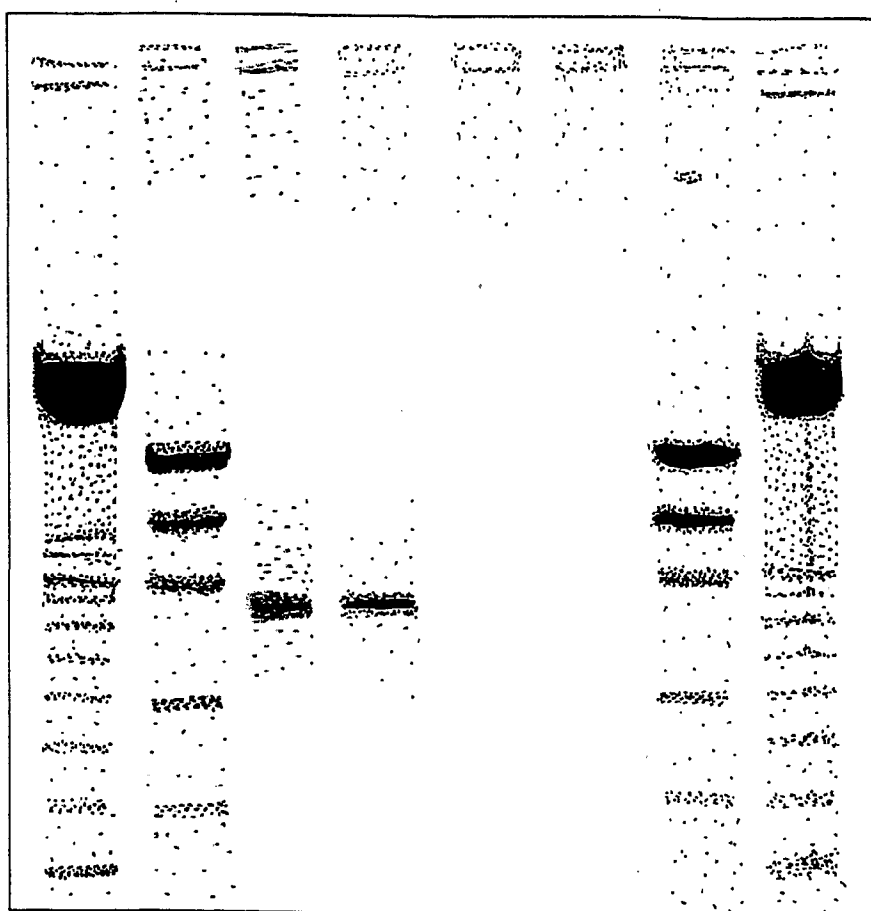


FIG. 2

*FIG. 3*

*FIG. 4*

*FIG. 5*

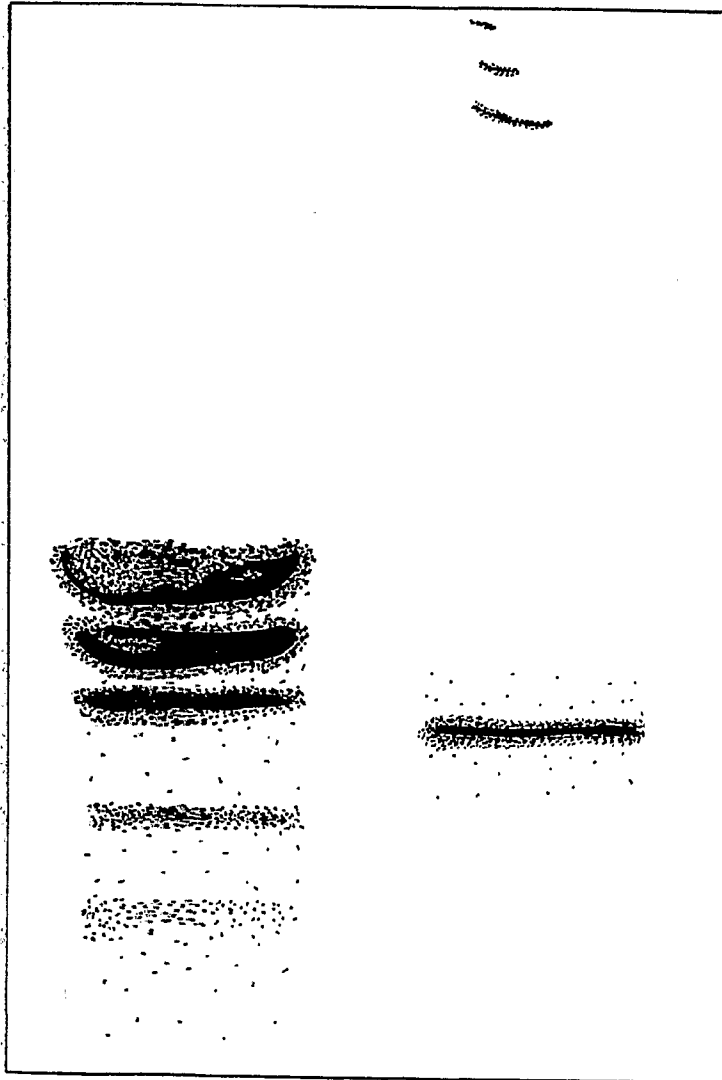


FIG. 6

Table 1: Cleavage of 75 human light chains.

Enzyme	Recognition*	Nch	Ns	Planned location of site
AfeI	AGCgct	0	0	
AflII	Cttaag	0	0	HC FR3
AgeI	Accggt	0	0	
AscI	GGcgcgcc	0	0	After LC
BglII	Agatct	0	0	
BsiWI	Cgtacg	0	0	
BspDI	ATcgat	0	0	
BssHII	Gcgcg	0	0	
BstBI	TTcgaa	0	0	
DraIII	CACNNNgtg	0	0	
EagI	Cggccg	0	0	
FseI	GGCCGGcc	0	0	
FspI	TGCgca	0	0	
HpaI	GTTaac	0	0	
MfeI	Caattg	0	0	HC FR1
MluI	Acgcgt	0	0	
NcoI	Ccatgg	0	0	Heavy chain signal
NheI	Gctagc	0	0	HC/anchor linker
NotI	GCggccgc	0	0	In linker after HC
NruI	TCGcga	0	0	
PacI	TTAATtaa	0	0	
PmeI	GTTTaaac	0	0	
PmlI	CACgtg	0	0	
PvuI	CGATcg	0	0	
SacII	CCGCgg	0	0	
SalI	Gtcgac	0	0	
SfiI	GGCCNNNNnggcc	0	0	Heavy Chain signal
SgfI	GCGATcgc	0	0	
SnaBI	TACgta	0	0	
StuI	AGGcct	0	0	
XbaI	Tctaga	0	0	HC FR3
AatII	GACGTc	1	1	
AclI	AAcggt	1	1	
AseI	ATtaat	1	1	
BsmI	GAATGCN	1	1	
BspEI	Tccgga	1	1	HC FR1
BstXI	CCANNNNntgg	1	1	HC FR2
DrdI	GACNNNNnngtc	1	1	
HindIII	Aagctt	1	1	
PciI	Acatgt	1	1	
SapI	gaagagc	1	1	
ScaI	AGTact	1	1	
SexAI	Accwgtt	1	1	
SpeI	Actagt	1	1	
TliI	Ctcgag	1	1	
XhoI	Ctcgag	1	1	
BcgI	cgannnnntgc	2	2	
BlpI	GCtnagc	2	2	
BssSI	Ctcgtg	2	2	
BstAPI	GCANNNNntgc	2	2	
EspI	GCtnagc	2	2	
KasI	Gcgccc	2	2	
PflMI	CCANNNNntgg	2	2	
XmnI	GAANNnttc	2	2	

ApaLI	Gtgcac	3	3	LC signal seq
NaeI	GCCggc	3	3	
NgoMI	Gccggc	3	3	
PvuII	CAGctg	3	3	
RsrII	CGgwccg	3	3	
BsrBI	GAGcgg	4	4	
BsrDI	GCAATGNNn	4	4	
BstZl7I	GTAtac	4	4	
EcoRI	Gaattc	4	4	
SphI	GCATGc	4	4	
SspI	AATatt	4	4	
AccI	GTmkac	5	5	
BclI	Tgatca	5	5	
BsmBI	Nnnnnngagacg	5	5	
BsrGI	Tgtaca	5	5	
DraI	TTTaaa	6	6	
NdeI	CAtatg	6	6	HC FR4
SwaI	ATTTaaat	6	6	
BamHI	Ggatcc	7	7	
SacI	GAGCTc	7	7	
BciVI	GTATCCNNNNNN	8	8	
BsaBI	GATNNnnatc	8	8	
NsiI	ATGCAt	8	8	
Bsp120I	Gggccc	9	9	CH1
ApaI	GGGCCc	9	9	CH1
PspOoMI	Gggccc	9	9	
BspHI	Tcatga	9	11	
EcoRV	GATatc	9	9	
AhdI	GACNNNnngtc	11	11	
BbsI	GAAGAC	11	14	
PsiI	TTATAa	12	12	
BsaI	GGTCTCNnnnn	13	15	
XmaI	Cccggg	13	14	
AvaI	Cycgrg	14	16	
BglI	GCCNNNNnggc	14	17	
AlwNI	CAGNNNctg	16	16	
BspMI	ACCTGC	17	19	
XcmI	CCANNNNNnnnntgg	17	26	
BstEII	Ggtnacc	19	22	HC FR4
Sse8387I	CCTGCAGg	20	20	
AvrII	Cctagg	22	22	
HincII	GTYrac	22	22	
BsgI	GTGCAG	27	29	
MscI	TGGcca	30	34	
BseRI	NNnnnnnnnnctcctc	32	35	
Bsu36I	CCtnagg	35	37	
PstI	CTGCAg	35	40	
EciI	nnnnnnnnntccgcc	38	40	
PpuMI	RGgwccy	41	50	
StyI	Ccwwgg	44	73	
EcoO109I	RGgnccy	46	70	
Acc65I	Ggtacc	50	51	
KpnI	GGTACc	50	51	
BpmI	ctccag	53	82	
AvaII	Ggwcc	71	124	

* cleavage occurs in the top strand after the last upper-case base. For REs

that cut palindromic sequences, the lower strand is cut at the symmetrical site.

Table 2: Cleavage of 79 human heavy chains

Enzyme	Recognition	Nch	Ns	Planned location of site
AfeI	AGCgct	0	0	
AflII	Cttaag	0	0	HC FR3
AscI	GGGcgccc	0	0	After LC
BsiWI	Cgtacg	0	0	
BspDI	ATcgat	0	0	
BssHII	Gcgcg	0	0	
FseI	GGCCGGcc	0	0	
HpaI	GTTaac	0	0	
NheI	Gctagc	0	0	HC Linker
NotI	GCggccgc	0	0	In linker, HC/anchor
NruI	TCGcga	0	0	
NsiI	ATGCAt	0	0	
PacI	TTAATtaa	0	0	
PciI	Acatgt	0	0	
PmeI	GTTTaaac	0	0	
PvuI	CGATcg	0	0	
RsrII	CGgwccg	0	0	
SapI	gaagagc	0	0	
SfiI	GGCCNNNNnggcc	0	0	HC signal seq
SgfI	GCGATcgc	0	0	
SwaI	ATTTaaat	0	0	
AclI	AACgtt	1	1	
AgeI	Accggt	1	1	
AseI	ATtaat	1	1	
AvrII	Cctagg	1	1	
BsmI	GAATGCN	1	1	
BsrBI	GAGcgg	1	1	
BsrDI	GCAATGNNn	1	1	
DraI	TTTaaa	1	1	
FspI	TGCgca	1	1	
HindIII	Aagctt	1	1	
MfeI	Caattg	1	1	HC FR1
NaeI	GCCggc	1	1	
NgoMI	Gccggc	1	1	
SpeI	Actagt	1	1	
Acc65I	Ggtacc	2	2	
BstBI	TTcgaa	2	2	
KpnI	GGTACc	2	2	
MluI	Acgcgt	2	2	
NcoI	Ccatgg	2	2	In HC signal seq
NdeI	CAtatg	2	2	HC FR4
PmlI	CACgtg	2	2	
XcmI	CCANNNNNnnnttg	2	2	
BcgI	cgannnnntgc	3	3	
BclI	Tgatca	3	3	
BglI	GCCNNNNnggc	3	3	
BsaBI	GATNNnnatc	3	3	
BsrGI	Tgtaca	3	3	
SnaBI	TACgta	3	3	
Sse8387I	CCTGCagg	3	3	

ApaLI	Gtgcac	4	4	LC Signal/FR1
BspHI	Tcatga	4	4	
BssSI	Ctcgtg	4	4	
PsiI	TTAtaa	4	5	
SphI	GCATGc	4	4	
AhdI	GACNNNnngtc	5	5	
BspEI	Tccgga	5	5	HC FR1
MscI	TGGcca	5	5	
SacI	GAGCTc	5	5	
ScaI	AGTact	5	5	
SexAI	Accwgg	5	6	
SspI	AATatt	5	5	
TliI	Ctcgag	5	5	
XhoI	Ctcgag	5	5	
BbsI	GAAGAC	7	8	
BstAPI	GCANNNNntgc	7	8	
BstZ17I	GTAtac	7	7	
EcoRV	GATatc	7	7	
EcoRI	Gaattc	8	8	
BlpI	GCtnagc	9	9	
Bsu36I	CCtnagg	9	9	
DraIII	CACNNNgtg	9	9	
EspI	GCtnagc	9	9	
StuI	AGGcct	9	13	
XbaI	Tctaga	9	9	HC FR3
Bsp120I	Gggccc	10	11	CH1
ApaI	GGGCCc	10	11	CH1
PspOoMI	Gggccc	10	11	
BciVI	GTATCCNNNNNN	11	11	
SalI	Gtcgac	11	12	
DrdI	GACNNNNnngtc	12	12	
KasI	Ggcgcc	12	12	
XmaI	Cccggg	12	14	
BglII	Agatct	14	14	
HincII	GTYrac	16	18	
BamHI	Ggatec	17	17	
PflMI	CCANNNNntgg	17	18	
BsmBI	Nnnnnngagacg	18	21	
BstXI	CCANNNNNntgg	18	19	HC FR2
XmnI	GAANNnnttc	18	18	
SacII	CCGCgg	19	19	
PstI	CTGCAG	20	24	
PvuII	CAGctg	20	22	
AvaI	Cycgrg	21	24	
EagI	Cggccg	21	22	
AatII	GACGTc	22	22	
BspMI	ACCTGC	27	33	
AccI	GTmkac	30	43	
StyI	Ccwwgg	36	49	
AlwNI	CAGNNNctg	38	44	
BsaI	GGTCTCNnnnn	38	44	
PpuMI	RGgwccy	43	46	
BsgI	GTGCAG	44	54	
BseRI	NNnnnnnnnnnctcctc	48	60	
EciI	nnnnnnnnntccgcc	52	57	
BstEII	Ggtnacc	54	61	HC Fr4, 47/79 have one
EcoO109I	RGgnccy	54	86	

BpmI	ctccag	60	121
Avall	Ggwcc	71	140


```

3'- gtGTAGGcac\ (SEQ ID NO:23)
      |caCATCCgtg/
5'-gag|tctc-actgagc
Substrate 3'-...ctc-agag|tgactcg...-5' (SEQ ID NO:24)

```


Table 8: Matches to URE FR3 adapters in 79 human HC.

A. List of Heavy-chains genes sampled

AF008566	af103343	HSA235676	HSU92452	HSZ93860
AF035043	AF103367	HSA235675	HSU94412	HSZ93863
AF103026	AF103368	HSA235674	HSU94415	MCOMFRAA
af103033	AF103369	HSA235673	HSU94416	MCOMFRVA
AF103061	AF103370	HSA240559	HSU94417	S82745
Af103072	af103371	HSCB201	HSU94418	S82764
af103078	AF103372	HSIGGVHC	HSU96389	S83240
AF103099	AF158381	HSU44791	HSU96391	SABVH369
AF103102	E05213	HSU44793	HSU96392	SADEIGVH
AF103103	E05886	HSU82771	HSU96395	SAH2IGVH
AF103174	E05887	HSU82949	HSZ93849	SDA3IGVH
AF103186	HSA235661	HSU82950	HSZ93850	SIGVHTTD
af103187	HSA235664	HSU82952	HSZ93851	SUK4IGVH
AF103195	HSA235660	HSU82961	HSZ93853	
af103277	HSA235659	HSU86522	HSZ93855	
af103286	HSA235678	HSU86523	HSZ93857	
AF103309	HSA235677			

Table 8 B. Testing all distinct GLGs from bases 89.1 to 93.2 of the heavy variable domain

Id	Nb	0	1	2	3	4		SEQ ID NO:
1	38	15	11	10	0	2	Seq1 gtgtattactgtgc	25
2	19	7	6	4	2	0	Seq2 gtAtattactgtgc	26
3	1	0	0	1	0	0	Seq3 gtgtattactgtAA	27
4	7	1	5	1	0	0	Seq4 gtgtattactgtAc	28
5	0	0	0	0	0	0	Seq5 Ttgtattactgtgc	29
6	0	0	0	0	0	0	Seq6 TtgtatCactgtgc	30
7	3	1	0	1	1	0	Seq7 ACAatattactgtgc	31
8	2	0	2	0	0	0	Seq8 ACgtattactgtgc	32
9	9	2	2	4	1	0	Seq9 ATgtattactgtgc	33
Group		26	26	21	4	2		
Cumulative		26	52	73	77	79		

Table 8C Most important URE recognition seqs in FR3 Heavy

1	VHSzy1	GTGtattactgtgc	(ON_SHC103)	(SEQ ID NO:25)
2	VHSzy2	GTAtattactgtgc	(ON_SHC323)	(SEQ ID NO:26)
3	VHSzy4	GTGtattactgtac	(ON_SHC349)	(SEQ ID NO:28)
4	VHSzy9	ATGtattactgtgc	(ON_SHC5a)	(SEQ ID NO:33)

Table 8D, testing 79 human HC V genes with four probes

Number of sequences..... 79

Number of bases..... 29143

		Number of mismatches								
Id	Best	0	1	2	3	4	5			
1	39	15	11	10	1	2	0	Seq1	gtgtattactgtgc	(SEQ ID NO:25)
2	22	7	6	5	3	0	1	Seq2	gtAtattactgtgc	(SEQ ID NO:26)
3	7	1	5	1	0	0	0	Seq4	gtgtattactgtAc	(SEQ ID NO:28)
4	11	2	4	4	1	0	0	Seq9	ATgtattactgtgc	(SEQ ID NO:33)
Group		25	26	20	5	2				
Cumulative		25	51	71	76	78				

One sequence has five mismatches with sequences 2, 4, and 9; it is scored as best for 2.

Id is the number of the adapter.

Best is the number of sequence for which the identified adapter was the best available.

The rest of the table shows how well the sequences match the adapters. For example, there are 11 sequences that match VHSzy1(Id=1) with 2 mismatches and are worse for all other adapters. In this sample, 90% come within 2 bases of one of the four adapters.

Table 130: PCR primers for amplification of human Ab genes

(HuIgMFOR) 5'-tgg aag agg cac gtt ctt ttc ttt-3'
 30 ! (HuIgMFOREtop) 5'-aaa gaa aag aac gtg cct ctt cca-3' = reverse complement
 (HuCkFOR) 5'-aca ctc tcc cct gtt gaa gct ctt-3'
 (HuCL2FOR) 5'-tga aca ttc tgt agg ggc cac tg-3'
 (HuCL7FOR) 5'-aga gca ttc tgc agg ggc cac tg-3'
 ! Kappa
 35 (CKForeAsc) 5'-acc gcc tcc acc ggg cgc gcc tta tta aca ctc tcc cct gtt-
 gaa gct ctt-3'
 (CL2ForeAsc) 5'-acc gcc tcc acc ggg cgc gcc tta tta tga aca ttc tgt-
 agg ggc cac tg-3'
 (CL7ForeAsc) 5'-acc gcc tcc acc ggg cgc gcc tta tta aga gca ttc tgc-
 40 agg ggc cac tg-3'

Table 195: Human GLG FR3 sequences

45 ! VH1
 ! 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80

agg gtc acc atg acc agg gac acg tcc atc agc aca gcc tac atg
 ! 81 82 82a 82b 82c 83 84 85 86 87 88 89 90 91 92
 gag ctg agc agg ctg aga tct gac gac acg gcc gtg tat tac tgt
 ! 93 94 95
 5 gcg aga ga ! 1-02# 1
 aga gtc acc att acc agg gac aca tcc gcg agc aca gcc tac atg
 gag ctg agc agc ctg aga tct gaa gac acg gct gtg tat tac tgt
 gcg aga ga ! 1-03# 2
 10 aga gtc acc atg acc agg aac acc tcc ata agc aca gcc tac atg
 gag ctg agc agc ctg aga tct gag gac acg gcc gtg tat tac tgt
 gcg aga gg ! 1-08# 3
 aga gtc acc atg acc aca gac aca tcc acg agc aca gcc tac atg
 gag ctg agg agc ctg aga tct gac gac acg gcc gtg tat tac tgt
 gcg aga ga ! 1-18# 4
 15 aga gtc acc atg acc gag gac aca tct aca gac aca gcc tac atg
 gag ctg agc agc ctg aga tct gag gac acg gcc gtg tat tac tgt
 gca aca ga ! 1-24# 5
 aga gtc acc att acc agg gac agg tct atg agc aca gcc tac atg
 gag ctg agc agc ctg aga tct gag gac aca gcc atg tat tac tgt
 20 gca aga ta ! 1-45# 6
 aga gtc acc atg acc agg gac acg tcc acg agc aca gtc tac atg
 gag ctg agc agc ctg aga tct gag gac acg gcc gtg tat tac tgt
 gcg aga ga ! 1-46# 7

aga gtc acc att acc agg gac atg tcc aca agc aca gcc tac atg
gag ctg agc agc ctg aga tcc gag gac acg gcc gtg tat tac tgt
gcg gca ga ! 1-58# 8
5 aga gtc acg att acc gcg gac gaa tcc acg agc aca gcc tac atg
gag ctg agc agc ctg aga tct gag gac acg gcc gtg tat tac tgt
gcg aga ga ! 1-69# 9
aga gtc acg att acc gcg gac aaa tcc acg agc aca gcc tac atg
gag ctg agc agc ctg aga tct gag gac acg gcc gtg tat tac tgt
gcg aga ga ! 1-e# 10
10 aga gtc acc ata acc gcg gac acg tct aca gac aca gcc tac atg
gag ctg agc agc ctg aga tct gag gac acg gcc gtg tat tac tgt
gca aca ga ! 1-f# 11
! VH2
15 agg ctc acc atc acc aag gac acc tcc aaa aac cag gtg gtc ctt
aca atg acc aac atg gac cct gtg gac aca gcc aca tat tac tgt
gca cac aga c! 2-05# 12
agg ctc acc atc tcc aag gac acc tcc aaa agc cag gtg gtc ctt
acc atg acc aac atg gac cct gtg gac aca gcc aca tat tac tgt
gca cgg ata c! 2-26# 13
20 agg ctc acc atc tcc aag gac acc tcc aaa aac cag gtg gtc ctt
aca atg acc aac atg gac cct gtg gac aca gcc acg tat tac tgt
gca cgg ata c! 2-70# 14
! VH3
25 cga ttc acc atc tcc aga gac aac gcc aag aac tca ctg tat ctg
caa atg aac agc ctg aga gcc gag gac acg gct gtg tat tac tgt
gcg aga ga ! 3-07# 15
cga ttc acc atc tcc aga gac aac gcc aag aac tcc ctg tat ctg
caa atg aac agt ctg aga gct gag gac acg gcc ttg tat tac tgt
gca aaa gat a! 3-09#16
30 cga ttc acc atc tcc agg gac aac gcc aag aac tca ctg tat ctg
caa atg aac agc ctg aga gcc gag gac acg gcc gtg tat tac tgt
gcg aga ga ! 3-11# 17
cga ttc acc atc tcc aga gaa aat gcc aag aac tcc ttg tat ctt
caa atg aac agc ctg aga gcc ggg gac acg gct gtg tat tac tgt
35 gca aga ga ! 3-13# 18
aga ttc acc atc tca aga gat gat tca aaa aac acg ctg tat ctg
caa atg aac agc ctg aaa acc gag gac aca gcc gtg tat tac tgt
acc aca ga ! 3-15# 19
cga ttc acc atc tcc aga gac aac gcc aag aac tcc ctg tat ctg

caa atg aac agt ctg aga gcc gag gac acg gcc ttg tat cac tgt
gcg aga ga ! 3-20# 20
cga ttc acc atc tcc aga gac aac gcc aag aac tca ctg tat ctg
caa atg aac agc ctg aga gcc gag gac acg gct gtg tat tac tgt
gcg aga ga ! 3-21# 21
cgg ttc acc atc tcc aga gac aat tcc aag aac acg ctg tat ctg
caa atg aac agc ctg aga gcc gag gac acg gcc gta tat tac tgt
gcg aaa ga ! 3-23# 22
cga ttc acc atc tcc aga gac aat tcc aag aac acg ctg tat ctg
caa atg aac agc ctg aga gct gag gac acg gct gtg tat tac tgt
gcg aaa ga ! 3-30# 23
cga ttc acc atc tcc aga gac aat tcc aag aac acg ctg tat ctg
caa atg aac agc ctg aga gct gag gac acg gct gtg tat tac tgt
gcg aga ga ! 3303# 24
cga ttc acc atc tcc aga gac aat tcc aag aac acg ctg tat ctg
caa atg aac agc ctg aga gct gag gac acg gct gtg tat tac tgt
gcg aaa ga ! 3305# 25
cga ttc acc atc tcc aga gac aat tcc aag aac acg ctg tat ctg
caa atg aac agc ctg aga gcc gag gac acg gct gtg tat tac tgt
gcg aga ga ! 3-33# 26
cga ttc acc atc tcc aga gac aac agc aaa aac tcc ctg tat ctg
caa atg aac agt ctg aga act gag gac acc gcc ttg tat tac tgt
gca aaa gat a! 3-43#27
cga ttc acc atc tcc aga gac aat gcc aag aac tca ctg tat ctg
caa atg aac agc ctg aga gac gag gac acg gct gtg tat tac tgt
gcg aga ga ! 3-48# 28
aga ttc acc atc tca aga gat ggt tcc aaa agc atc gcc tat ctg
caa atg aac agc ctg aaa acc gag gac aca gcc gtg tat tac tgt
act aga ga ! 3-49# 29
cga ttc acc atc tcc aga gac aat tcc aag aac acg ctg tat ctt
caa atg aac agc ctg aga gcc gag gac acg gcc gtg tat tac tgt
gcg aga ga ! 3-53# 30
aga ttc acc atc tcc aga gac aat tcc aag aac acg ctg tat ctt
caa atg ggc agc ctg aga gct gag gac atg gct gtg tat tac tgt
gcg aga ga ! 3-64# 31
aga ttc acc atc tcc aga gac aat tcc aag aac acg ctg tat ctt
caa atg aac agc ctg aga gct gag gac acg gct gtg tat tac tgt
gcg aga ga ! 3-66# 32
aga ttc acc atc tca aga gat gat tca aag aac tca ctg tat ctg

caa atg aac agc ctg aaa acc gag gac acg gcc gtg tat tac tgt
gct aga ga ! 3-72# 33
agg ttc acc atc tcc aga gat gat tca aag aac acg gcg tat ctg
caa atg aac agc ctg aaa acc gag gac acg gcc gtg tat tac tgt
5 act aga ca ! 3-73# 34
cga ttc acc atc tcc aga gac aac gcc aag aac acg ctg tat ctg
caa atg aac agt ctg aga gcc gag gac acg gct gtg tat tac tgt
gca aga ga ! 3-74# 35
aga ttc acc atc tcc aga gac aat tcc aag aac acg ctg cat ctt
10 caa atg aac agc ctg aga gct gag gac acg gct gtg tat tac tgt
aag aaa ga ! 3-d# 36
! VH4
cga gtc acc ata tca gta gac aag tcc aag aac cag ttc tcc ctg
aag ctg agc tct gtg acc gcc gcg gac acg gcc gtg tat tac tgt
15 gcg aga ga ! 4-04# 37
cga gtc acc atg tca gta gac acg tcc aag aac cag ttc tcc ctg
aag ctg agc tct gtg acc gcc gtg gac acg gcc gtg tat tac tgt
gcg aga aa ! 4-28# 38
cga gtt acc ata tca gta gac acg tct aag aac cag ttc tcc ctg
20 aag ctg agc tct gtg act gcc gcg gac acg gcc gtg tat tac tgt
gcg aga ga ! 4301# 39
cga gtc acc ata tca gta gac agg tcc aag aac cag ttc tcc ctg
aag ctg agc tct gtg acc gcc gcg gac acg gcc gtg tat tac tgt
gcc aga ga ! 4302# 40
25 cga gtt acc ata tca gta gac acg tcc aag aac cag ttc tcc ctg
aag ctg agc tct gtg act gcc gca gac acg gcc gtg tat tac tgt
gcc aga ga ! 4304# 41
cga gtt acc ata tca gta gac acg tct aag aac cag ttc tcc ctg
aag ctg agc tct gtg act gcc gcg gac acg gcc gtg tat tac tgt
30 gcg aga ga ! 4-31# 42
cga gtc acc ata tca gta gac acg tcc aag aac cag ttc tcc ctg
aag ctg agc tct gtg acc gcc gcg gac acg gct gtg tat tac tgt
gcg aga ga ! 4-34# 43
cga gtc acc ata tcc gta gac acg tcc aag aac cag ttc tcc ctg
35 aag ctg agc tct gtg acc gcc gca gac acg gct gtg tat tac tgt
gcg aga ca ! 4-39# 44
cga gtc acc ata tca gta gac acg tcc aag aac cag ttc tcc ctg
aag ctg agc tct gtg acc gct gcg gac acg gcc gtg tat tac tgt
gcg aga ga ! 4-59# 45

cga gtc acc ata tca gta gac acg tcc aag aac cag ttc tcc ctg
aag ctg agc tct gtg acc gct gcg gac acg gcc gtg tat tac tgt
gcg aga ga ! 4-61# 46

cga gtc acc ata tca gta gac acg tcc aag aac cag ttc tcc ctg
aag ctg agc tct gtg acc gcc gca gac acg gcc gtg tat tac tgt
gcg aga ga ! 4-b# 47

! VH5

cag gtc acc atc tca gcc gac aag tcc atc agc acc gcc tac ctg
cag tgg agc agc ctg aag gcc tcg gac acc gcc atg tat tac tgt
gcg aga ca ! 5-51# 48

cac gtc acc atc tca gct gac aag tcc atc agc act gcc tac ctg
cag tgg agc agc ctg aag gcc tcg gac acc gcc atg tat tac tgt
gcg aga ! 5-a# 49

! VH6

cga ata acc atc aac cca gac aca tcc aag aac cag ttc tcc ctg
cag ctg aac tct gtg act ccc gag gac acg gct gtg tat tac tgt
gca aga ga ! 6-1# 50

! VH7

cgg ttt gtc ttc tcc ttg gac acc tct gtc agc acg gca tat ctg
cag atc tgc agc cta aag gct gag gac act gcc gtg tat tac tgt
gcg aga ga ! 74.1# 51

J

Table 250: REaptors, Extenders, and Bridges used for Cleavage and Capture of Human Heavy Chains in FR3.

A: HpyCH4V Probes of actual human HC genes

!HpyCH4V in FR3 of human HC, bases 35-56; only those with TGca site
TGca;10,

RE recognition:tgca

of length 4 is expected at 10

1

6-1 agttctccctgcagctgaactc

```

2          3-11,3-07,3-21,3-72,3-48 cactgtatctgcaaatgaacag
3          3-09,3-43,3-20 ccctgtatctgcaaatgaacag
4          5-51 ccgcctacctgcagtgaggagcag
5 3-15,3-30,3-30.5,3-30.3,3-74,3-23,3-33 cgctgtatctgcaaatgaacag
5 6          7-4.1 cggcatatctgcagatctgcag
7          3-73 cggcgtatctgcaaatgaacag
8          5-a ctgcctacctgcagtgaggagcag
9          3-49 tcgcctatctgcaaatgaacag

```

10 **B: HpyCH4V REaptors, Extenders, and Bridges**

B.1 REaptors

! Cutting HC lower strand:

! TmKeller for 100 mM NaCl, zero formamide

! Eaptors for cleavage

		T_m^W	T_m^K
15	(ON_HCFR36-1) 5'-agttctcccTGCAgctgaactc-3'	68.0	64.5
	(ON_HCFR36-1A) 5'-ttctcccTGCAgctgaactc-3'	62.0	62.5
	(ON_HCFR36-1B) 5'-ttctcccTGCAgctgaac-3'	56.0	59.9
	(ON_HCFR33-15) 5'-cgctgtatcTGCAaatgaacag-3'	64.0	60.8
	(ON_HCFR33-15A) 5'-ctgtatcTGCAaatgaacag-3'	56.0	56.3
20	(ON_HCFR33-15B) 5'-ctgtatcTGCAaatgaac-3'	50.0	53.1
	(ON_HCFR33-11) 5'-cactgtatcTGCAaatgaacag-3'	62.0	58.9
	(ON_HCFR35-51) 5'-ccgcctaccTGCAgtggagcag-3'	74.0	70.1

!

B.2 Segment of synthetic 3-23 gene into which captured CDR3 is to be cloned

```

25 ! XbaI...
! D323* cgCttcacTaag tct aga gac aaC tctT aag aaT acT ctC taC
! scab..... designed gene 3-23 gene.....
!
```

```

30 ! HpyCH4V
! .. .. AflII...
! Ttg caG atg aac agc TtA agG . . .
! .....
!
```

B.3 Extender and Bridges

35 ! Extender (bottom strand):

!

(ON_HCHpyEx01) 5'-cAAGTAgAgAgTATTcTTAgAgTTgTcTcTAgAcTTAgTgAAgcg-3'

! ON_HCHpyEx01 is the reverse complement of

! 5'-cgCttcacTaag tctT aga gac aaC tctT aag aaT acT ctC taC Ttg -3'

40 !

! Bridges (top strand, 9-base overlap):

!

(ON_HCHpyBr016-1) 5'-cgCttcacTaag tcT aga gac aaC tcT aag-
aaT acT ctC taC Ttg CAgctgaac-3' {3'-term C is blocked}

!

5 ! 3-15 et al. + 3-11

(ON_HCHpyBr023-15) 5'-cgCttcacTaag tcT aga gac aaC tcT aag-
aaT acT ctC taC Ttg CAaatgaac-3' {3'-term C is blocked}

!

! 5-51

10 (ON_HCHpyBr045-51) 5'-cgCttcacTaag tcT aga gac aaC tcT aag-
aaT acT ctC taC Ttg CAgtggagc-3' {3'-term C is blocked}

!

! PCR primer (top strand)

!

15 (ON_HCHpyPCR) 5'-cgCttcacTaag tcT aga gac-3'

!

C: BspI Probes from human HC GLGs

20	1	1-58,1-03,1-08,1-69,1-24,1-45,1-46,1-f,1-e	acatggaGCTGAGCagcctgag
	2		1-02 acatggaGCTGAGCagcctgag
	3		1-18 acatggagctgaggagcctgag
	4		5-51,5-a acctgcagtggagcagcctgaa
25	5	3-15,3-73,3-49,3-72	atctgcaaatgaacagcctgaa
	6	3303,3-33,3-07,3-11,3-30,3-21,3-23,3305,3-48	atctgcaaatgaacagcctgag
	7	3-20,3-74,3-09,3-43	atctgcaaatgaacagtctgag
	8		74.1 atctgcagatctgcagcctaaa
30	9	3-66,3-13,3-53,3-d	atcttcaaatgaacagcctgag
	10		3-64 atcttcaaatgggcagcctgag
	11	4301,4-28,4302,4-04,4304,4-31,4-34,4-39,4-59,4-61,4-b	ccctgaaGCTGAGCtctgtgac
	12		6-1 ccctgcagctgaactctgtgac
40	13	2-70,2-05	tccttacaatgaccaacatgga
	14	2-26	tccttaccatgaccaacatgga

D: BspI REaptors, Extenders, and Bridges**35 D.1 REaptors**

		T_m^W	T_m^K
(BlpF3HC1-58)	5'-ac atg gaG CTG AGC agc ctg ag-3'	70	66.4
(BlpF3HC6-1)	5'-cc ctg aag ctg agc tct gtg ac-3'	70	66.4

! BlpF3HC6-1 matches 4-30.1, not 6-1.

40

D.2 Segment of synthetic 3-23 gene into which captured CDR3 is to be cloned

```

!
!                                     BlpI
!                                     . . . . .
!D323*   cgCttcacTaag TCT AGA gac aaC tcT aag aaT acT ctC taC Ttg caG atg aac
!
!                                     AflIII...
!                                     agC TTA AGG
!

```

D.3 Extender and Bridges

! Bridges

(BlpF3Br1) 5'-cgCttcacTcag tcT aga gaT aaC AGT aaA aaT acT TtG-
taC Ttg caG Ctg a|GC agc ctg-3'

(BlpF3Br2) 5'-cgCttcacTcag tcT aga gaT aaC AGT aaA aaT acT TtG-
taC Ttg caG Ctg a|gc tct gtg-3'

! | lower strand is cut here

! Extender

(BlpF3Ext) 5'-

TcAgcTgcAAgTAcAAAGTATTTTAcTgTTATcTcTAgAcTgAgTgAAgcg-3'

! BlpF3Ext is the reverse complement of:

! 5'-cgCttcacTcag tcT aga gaT aaC AGT aaA aaT acT TtG taC Ttg caG Ctg a-3'

!

(BlpF3PCR) 5'-cgCttcacTcag tcT aga gaT aaC-3'

E: HpyCH4III Distinct GLG sequences surrounding site, bases 77-98

1	102#1,118#4,146#7,169#9,1e#10,311#17,353#30,404#37,4301	ccgtgtattactgtgcgagaga
2	103#2,307#15,321#21,3303#24,333#26,348#28,364#31,366#32	ctgtgtattactgtgcgagaga
3	108#3	ccgtgtattactgtgcgagagg
4	124#5,1f#11	ccgtgtattactgtgcaacaga
5	145#6	ccatgtattactgtgcaagata
6	158#8	ccgtgtattactgtgcggcaga
7	205#12	ccacatattactgtgcacacag
8	226#13	ccacatattactgtgcacggat
9	270#14	ccacgtattactgtgcacggat
10	309#16,343#27	ccttgtattactgtgcaaaaga
11	313#18,374#35,61#50	ctgtgtattactgtgcaagaga
12	315#19	ccgtgtattactgtgcaacaga
13	320#20	ccttgtatcactgtgcgagaga
14	323#22	ccgtatattactgtgcgaaaga
15	330#23,3305#25	ctgtgtattactgtgcgaaaga
16	349#29	cogtgtattactgtgactagaga
17	372#33	cogtgtattactgtgctagaga
18	373#34	ccgtgtattactgtgactagaca
19	3d#36	ctgtgtattactgtgaagaaaga
20	428#38	ccgtgtattactgtgcgagaaa
21	4302#40,4304#41	ccgtgtattactgtgcgagaga
22	439#44	ctgtgtattactgtgcgagaca
23	551#48	ccatgtattactgtgcgagaca

F: HpyCH4III REaptors, Extenders, and Bridges**F.1 REaptors**

! ONs for cleavage of HC(lower) in FR3(bases 77-97)

! For cleavage with HpyCH4III, Bst4CI, or TaaI

! cleavage is in lower chain before base 88.

!		77	788	888	888	889	999	999	9		
!		78	901	234	567	890	123	456	7	T_m^W	T_m^K
(H43.77.97.1-02#1)	5'-cc	gtg	tat	tAC	TGT	gcg	aga	g-3'		64	62.6
(H43.77.97.1-03#2)	5'-c	gtg	tat	tAC	TGT	gcg	aga	g-3'		62	60.6
(H43.77.97.108#3)	5'-cc	gtg	tat	tAC	TGT	gcg	aga	g-3'		64	62.6
(H43.77.97.323#22)	5'-cc	gt	tat	tac	tgt	gcg	aaa	g-3'		60	58.7
(H43.77.97.330#23)	5'-c	gtg	tat	tac	tgt	gcg	aaa	g-3'		60	58.7
(H43.77.97.439#44)	5'-c	gtg	tat	tac	tgt	gcg	aga	-3'		62	60.6
(H43.77.97.551#48)	5'-cc	atg	tat	tac	tgt	gcg	aga	-3'		62	60.6
(H43.77.97.5a#49)	5'-cc	atg	tat	tAC	TGT	gcg	aga	-3'		58	58.3

F.2 Extender and Bridges

! XbaI and AflIII sites in bridges are bunged

(H43.XABr1) 5'-ggtgtagtga-

|TCT|AGT|gac|aac|tct|aag|aat|act|ctc|tac|ttg|cag|atg|-

|aac|agC|TTT|AGg|gct|gag|gac|aCT|GCA|Gtc|tac|tat|tgt|gcg|aga-3'

(H43.XABr2) 5'-ggtgtagtga-

|TCT|AGT|gac|aac|tct|aag|aat|act|ctc|tac|ttg|cag|atg|-

|aac|agC|TTT|AGg|gct|gag|gac|aCT|GCA|Gtc|tac|tat|tgt|gcg|aaa-3'

(H43.XAExt) 5'-ATAgTAgAcT gcAgTgTccT cAgcccTTAA gCTgTTcATc TgcAAgTAgA-
gAgTATTcTT AgAgTTgTcT cTAgATcAcT AcAcc-3'

!H43.XAExt is the reverse complement of

! 5'-ggtgtagtga-

! |TCT|AGA|gac|aac|tct|aag|aat|act|ctc|tac|ttg|cag|atg|-

! |aac|agC|TTA|AGg|gct|gag|gac|aCT|GCA|Gtc|tac|tat|-3'

(H43.XAPCR) 5'-ggtgtagtga |TCT|AGA|gac|aac-3'

! XbaI and AflIII sites in bridges are bunged

(H43.ABr1) 5'-ggtgtagtga-

|aac|agC|TTT|AGg|gct|gag|gac|aCT|GCA|Gtc|tac|tat|tgt|gcg|aga-3'

(H43.ABr2) 5'-ggtgtagtga-

|aac|agC|TTT|AGg|gct|gag|gac|aCT|GCA|Gtc|tac|tat|tgt|gcg|aaa-3'

(H43.AEExt) 5'-ATAgTAgAcTgcAgTgTccTcAgcccTTAAgcTgTTcAcTAcAcc-3'

!(H43.AExt) is the reverse complement of 5'-ggtgtagtga-

! |aac|agC|TTA|AGg|gct|gag|gac|aCT|GCA|Gtc|tac|tat -3'

(H43.APCR) 5'-ggtgtagtga |aac|agC|TTA|AGg|gct|g-3'

25

(FOKIact) 5'-cAcATccgTg TTgTT cAcgATgTg-3'

(VHEX881) 5'-AATAgTAGAc TgcAgTgTcc TcAgcccTTA AgcTgTTcAT cTgcAAgTAG-
AgAgTATtCT TAGAgTTgTc TcTAGACTTA gTgAAgcg-3'

! note that VHEX881 is the reverse complement of the ON below

! [RC] 5'-cgCttcacTaag-

! Scab.....

! Synthetic 3-23 as in Table 206

! |TCT|AGA|gac|aac|tct|aag|aat|act|ctc|tac|ttg|cag|atg|-

! XbaI...

! |aac|agC|TTA|AGg|gct|gag|gac|aCT|GCA|Gtc|tac|tat|t-3'

! AflII...

35 (VHBA881) 5'-cgCttcacTaag-

|TCT|AGA|gac|aac|tct|aag|aat|act|ctc|tac|ttg|cag|atg|-

|aac|agC|TTA|AGg|gct|gag|gac|aCT|GCA|Gtc|tac|tat|tgt gcg ag-3'

(VHBB881) 5'-cgCttcacTaag-

Table 510

(VH881PCR) 5'-cgCttcacTaaG|TCT|AGA|gac|aac -3'
|TCT|AGA|gac|aac|tct|aag|aat|act|ctc|tac|ttg|cag|atg|-
|aac|agC|TTA|AGg|gct|gag|gac|aCT|GCA|Gtc|tac|tat|tgt|Acg|ag-3'

Table 600: V3-23 VH framework with variegated codons shown

5'-ctg tct gaa cg gcc caq cgg gcc atg gcc
A Q P A M A
17 18 19 20 21 22

3'-gac aga ctt gc cgg gtc ggc cgg tac cgg
Scab.....Still.....
Ngoml.....
NcoI.....

FR1 (DP47/V3-23)-----

23 24 25 26 27 28 29 30
E V Q L L E S G
gaa|gtt|caa|tta|gag|tct|ggt|
gaa|gtt|caa|gtt|aac|aat|ctc|aga|cca|
ctt|caa|gtt|aac|aat|ctc|aga|cca|

53

-----FR1-----
31 32 33 34 35 36 37 38 39 40 41 42 43 44 45
G G L V Q P G G S L R L S C A
|ggc|ggt|ctt|gtt|cag|cgt|ggt|ggt|tct|tta|cgt|ctt|tct|tgc|gct|
|ccg|cca|gaa|caa|gtc|gga|cca|cca|aga|aat|gca|gaa|aga|acg|cga|

98

```

! Sites to be varied--->          ***      ***      ***
! -----FR1----->|...CDR1.....|-----FR2-----
! 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60
!   A  S  G  F  T  F  S  S  Y  A  M  S  W  V  R
! |qct|TCC|GGA|ttc|act|ttc|tct|tCG|TAC|Gct|atg|tct|tgg|gtt|cgC| 143
! |cga|agg|cct|aag|tga|aag|aga|agc|atg|cga|tac|aga|acc|caa|gcg|
!   | BspEI |           | BsiWI |           | BstXI.
!
!           Sites to be varies---> ***      ***      ***
! -----FR2----->|...CDR2.....
! 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75
!   Q  A  P  G  K  G  L  E  W  V  S  A  I  S  G
! |CAa|gct|cct|Ggt|aaa|ggt|ttg|gag|tgg|gtt|tct|gct|atc|tct|ggt| 188
! |gtt|cga|gga|cca|ttt|cca|aac|ctc|acc|caa|aga|cga|tag|aga|cca|
! ...BstXI
!
!           ***      ***
! .....CDR2.....|-----FR3-----
! 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90
!   S  G  G  S  T  Y  Y  A  D  S  V  K  G  R  F
! |tct|ggt|ggc|agt|act|tac|tat|gct|gac|tcc|gtt|aaa|ggt|cgc|ttc| 233
! |aga|cca|ccg|tca|tga|atg|ata|cga|ctg|agg|caa|ttt|cca|gcg|aag|
!
! -----FR3-----
! 91 92 93 94 95 96 97 98 99 100 101 102 103 104 105
!   T  I  S  R  D  N  S  K  N  T  L  Y  L  Q  M
! |act|atc|TCT|AGA|gac|aac|tct|aag|aat|act|ctc|tac|ttg|cag|atg| 278
! |tga|tag|aga|tct|ctg|ttg|aga|ttc|tta|tga|gag|atg|aac|gtc|tac|
!   | XbaI |
!
! -----FR3----->|
! 106 107 108 109 110 111 112 113 114 115 116 117 118 119 120
!   N  S  L  R  A  E  D  T  A  V  Y  Y  C  A  K
! |aac|agC|TTA|AGg|gct|gag|gac|aCT|GCA|Gtc|tac|tat|tgc|gct|aaa| 323
! |ttg|tog|aat|tcc|cga|ctc|ctg|tga|cgt|cag|atg|ata|acg|cga|ttt|
!   |AflII |           | PstI |
!
! .....CDR3.....|-----FR4-----
! 121 122 123 124 125 126 127 128 129 130 131 132 133 134 135
!   D  Y  E  G  T  G  Y  A  F  D  I  W  G  Q  G
! |gac|tat|gaa|ggt|act|ggt|tat|gct|ttc|gaC|ATA|TGg|ggt|caa|ggt| 368
! |ctg|ata|ctt|cca|tga|cca|ata|cga|aag|ctg|tat|acc|cca|gtt|cca|
!           | NdeI |
!
! -----FR4----->|
! 136 137 138 139 140 141 142
!   T  M  V  T  V  S  S
! |act|atG|GTC|ACC|gtc|tct|agt- 389
! |tga|tac|cag|tgg|cag|aga|tca-
!   | BstEII |
!
!           143 144 145 146 147 148 149 150 151 152
!           A  S  T  K  G  P  S  V  F  P
!           gcc tcc acc aaG GGC CCa tCG GTC TTC ccc-3' 419
!           cgg agg tgg ttc ccg ggt agc cag aag ggg-5'
!           Bsp120I.      BbsI...(2/2)
!           ApaI....
!
! (SFPRMET) 5'-ctg tct gaa cG GCC cag ccG-3'
! (TOPFR1A) 5'-ctg tct gaa cG GCC cag ccG GCC atg gcc-
!           gaa|gtt|CAA|TTG|tta|gag|tct|ggt|-
!           |ggc|ggt|ctt|gtt|cag|cct|ggt|ggt|tct|tta-3'
! (BOTFR1B) 3'-caa|gtc|gga|cca|cca|aga|aat|gca|gaa|aga|acg|cga|-
!           |cga|agg|cct|aag|tga|aag-5' ! bottom strand

```

```

(BOTFR2)  3'-acc|caa|gcg|-
           |ggt|cga|gga|cca|ttt|cca|aac|ctc|acc|caa|aga|-5' ! bottom strand
(BOTFR3)  3'- a|cga|ctg|agg|caa|ttt|cca|gcg|aag|-
           |tga|tag|aga|tct|ctg|ttg|aga|ttc|tta|tga|gag|atg|aac|gtc|tac|-
5         |ttg|tcg|aat|tcc|cga|ctc|ctg|tga-5'
(F06)     5'-gC|TTA|AGg|gct|gag|gac|aCT|GCA|Gtc|tac|tat|tgc|gct|aaa|-
           |gac|tat|gaa|ggt|act|ggt|tat|gct|ttc|gaC|ATA|TGg|ggt|c-3'
(BOTFR4)  3'-cga|aag|ctg|tat|acc|cca|ggt|cca|-
           |tga|tac|cag|tgg|cag|aga|tca-
10        cgg agg tgg ttc cgg ggt agc cag aag ggg-5' ! bottom strand
(BOTPRCPRIM)  3'-gg ttc cgg ggt agc cag aag ggg-5'
!
! CDR1 diversity
!
15 (ON-vgC1)  5'-gct|TCC|GGA|ttc|act|ttc|tct|<1>|TAC|<1>|atg|<1>|-
           ! CDR1.....6859
           |tgg|ggt|cgc|CAa|gct|ccT|GG-3'
!
! <1> stands for an equimolar mix of {ADEFHGHIKLMNPQSTVWY}; no C
20 ! (this is not a sequence)
!
! CDR2 diversity
!
25 (ON-vgC2)  5'-ggt|ttg|gag|tgg|ggt|tct|<2>|atc|<2>|<3>|-
           ! CDR2.....
           |tct|ggt|ggc|<1>|act|<1>|tat|gct|gac|tcc|ggt|aaa|gg-3'
           CDR2.....
!
! <1> is an equimolar mixture of {ADEFHGHIKLMNPQSTVWY}; no C
! <2> is an equimolar mixture of {YRWVGS}; no ACDEFHGHIKLMNPQT
30 ! <3> is an equimolar mixture of {PS}; no ACDEFHGHIKLMNPQSTVWY

```

Table 800 (new)

The following list of enzymes was taken from
<http://rebase.neb.com/cgi-bin/asymmlist>.

I have removed the enzymes that a) cut within the recognition, b) cut on both sides of the recognition, or c) have fewer than 2 bases between recognition and closest cut site.

REBASE Enzymes

04/13/2001

Type II restriction enzymes with asymmetric recognition sequences:

Enzymes	Recognition Sequence	Isoschizomers	Suppliers
AarI	CACCTGCNNNN [^] NNNN	-	Y
AceIII	CAGCTCNNNNNNNN [^] NNNN	-	-
Bbr7I	GAAGACNNNNNNNN [^] NNNN	-	-
BbvI	GCAGCNNNNNNNN [^] NNNN	-	Y
BbvII	GAAGACNN [^] NNNN	-	-
Bce83I	CTTGAGNNNNNNNNNNNNNN [^] NN	-	-
BceAI	ACGGCNNNNNNNNNNNN [^] NN	-	Y
BceFI	ACGGCNNNNNNNNNNNN [^] N	-	-
BciVI	GTATCCNNNNN [^] N	BfuI	Y
BfiI	ACTGGGNNNN [^] N	BmrI	Y
BinI	GGATCNNNN [^] N	-	-
BscAI	GCATCNNNN [^] NN	-	-
BseRI	GAGGAGNNNNNNNN [^] NN	-	Y
BsmFI	GGGACNNNNNNNNNN [^] NNNN	BspLU11III	Y
BspMI	ACCTGCNNNN [^] NNNN	Acc36I	Y
EciI	GGCGGANNNNNNNNNN [^] NN	-	Y
Eco57I	CTGAAGNNNNNNNNNNNNNN [^] NN	BspKT5I	Y
FauI	CCCGCNNNN [^] NN	BstFZ438I	Y
FokI	GGATGNNNNNNNN [^] NNNN	BstPZ418I	Y
GsuI	CTGGAGNNNNNNNNNNNNNN [^] NN	-	Y
HgaI	GACGCNNNN [^] NNNNN	-	Y
HphI	GGTGANNNNNNN [^] N	AsuHPI	Y
MboII	GAAGANNNNNNN [^] N	-	Y
MlyI	GAGTCNNNN [^] N	SchI	Y
MmeI	TCCRACNNNNNNNNNNNNNNNNNN [^] NN	-	-
MnlI	CCTCNNNNNN [^] N	-	Y
PleI	GAGTCNNNN [^] N	PpsI	Y
RleAI	CCCACANNNNNNNNNN [^] NNN	-	-
SfaNI	GCATCNNNN [^] NNNN	BspST5I	Y
SspD5I	GGTGANNNNNNNN [^] N	-	-
Sth132I	CCCGNNNN [^] NNNN	-	-
StsI	GGATGNNNNNNNNNN [^] NNNN	-	-
TaqII	GACCGANNNNNNNNNN [^] NN, CACCCANNNNNNNNNN [^] NN	-	-
Tth111II	CAARCANNNNNNNNN [^] NN	-	-
UbaPI	CGAACG	-	-

The notation is ^ means cut the upper strand and _ means cut the lower strand. If the upper and lower strand are cut at the same place, then only ^ appears.

Table 120: MALIA3, annotated

! MALIA3 9532 bases

```

!-----
1 aat gct act act att agt aga att gat gcc acc ttt tca gct cgc gcc
5 ! gene ii continued
49 cca aat gaa aat ata gct aaa cag gtt att gac cat ttg cga aat gta
97 tct aat ggt caa act aaa tct act cgt tcg cag aat tgg gaa tca_act
145 gtt aca tgg aat gaa act tcc aga cac cgt act tta gtt gca tat tta
193 aaa cat gtt gag cta cag cac cag att cag caa tta agc tct aag cca
10 241 tcc gca aaa atg acc tct tat caa aag gag caa tta aag gta ctc tct
289 aat cct gac ctg ttg gag ttt gct tcc ggt ctg gtt cgc ttt gaa gct
337 cga att aaa acg cga tat ttg aag tct ttc ggg ctt cct ctt aat ctt
385 ttt gat gca atc cgc ttt gct tct gac tat aat agt cag ggt aaa gac
433 ctg att ttt gat tta tgg tca ttc tcg ttt tct gaa ctg ttt aaa gca
15 481 ttt gag ggg gat tca ATG aat att tat gac gat tcc gca gta ttg gac
! RBS?..... Start gene x, ii continues
529 gct atc cag tct aaa cat ttt act att acc ccc tct ggc aaa act tct
577 ttt gca aaa gcc tct cgc tat ttt ggt ttt tat cgt cgt ctg gta aac
625 gag ggt tat gat agt gtt gct ctt act atg cct cgt aat tcc ttt tgg
20 673 cgt tat gta tct gca tta gtt gaa tgt ggt att cct aaa tct caa ctg
721 atg aat ctt tct acc tgt aat aat gtt gtt ccg tta gtt cgt ttt att
769 aac gta gat ttt tct tcc caa cgt cct gac tgg tat aat gag cca gtt
817 ctt aaa atc gca TAA
! End X & II
25 832 ggtaattca ca
!
! M1 E5 Q10 T15
843 ATG att aaa gtt gaa att aaa cca tct caa gcc caa ttt act act cgt
! Start gene V
30 !
! S17 S20 P25 E30
891 tct ggt gtt tct cgt cag ggc aag cct tat tca ctg aat gag cag ctt
!
! V35 E40 V45
35 939 tgt tac gtt gat ttg ggt aat gaa tat ccg gtt ctt gtc aag att act
!
! D50 A55 L60
987 ctt gat gaa ggt cag cca gcc tat gcg cct ggt cTG TAC Acc gtt cat
! BsrGI...

```

```

!           L65                V70                S75                R80
1035 ctg tcc tct ttc aaa gtt ggt cag ttc ggt tcc ctt atg att gac cgt
!
!
!           P85      K87 end of V
5  1083 ctg cgc ctc gtt ccg gct aag TAA C
!
!  1108 ATG gag cag gtc gcg gat ttc gac aca att tat cag gcg atg
!      Start gene VII
!
10 1150 ata caa atc tcc gtt gta ctt tgt ttc gcg ctt ggt ata atc
!
!
!           VII and IX overlap.
!           ..... S2  V3  L4  V5                S10
1192 gct ggg ggt caa agA TGA gt gtt tta gtg tat tct ttc gcc tct ttc gtt
15 !
!           End VII
!           |start IX
!           L13      W15                G20                T25                E29
1242 tta ggt tgg tgc ctt cgt agt ggc att acg tat ttt acc cgt tta atg gaa
!
20 1293 act tcc tc
!
!
!           .... stop of IX, IX and VIII overlap by four bases
1301 ATG aaa aag tct tta gtc ctc aaa gcc tct gta gcc gtt gct acc ctc
!      Start signal sequence of viii.
25 !
1349 gtt ccg atg ctg tct ttc gct gct gag ggt gac gat ccc gca aaa gcg
!
!           mature VIII ---->
1397 gcc ttt aac tcc ctg caa gcc tca gcg acc gaa tat atc ggt tat gcg
1445 tgg gcg atg gtt gtt gtc att
30 1466 gtc ggc gca act atc ggt atc aag ctg ttt aag
1499 aaa ttc acc tcg aaa gca ! 1515
!
!           ..... -35 ..
!
1517      agc tga taaaccgat acaattaaag gctccttttg
35 !
!           ..... -10 ...
!
1552 gagccttttt ttttGGAGAt ttt ! S.D. underlined
!
!           <----- III signal sequence ----->

```

```

!           M   K   K   L   L   F   A   I   P   L   V
1575 caac GTG aaa aaa tta tta ttc gca att cct tta gtt ! 1611
!
!           V   P   F   Y   S   H   S   A   Q
5  1612 gtt cct ttc tat tct cac aGT gcA Cag tCT
!
!                                     ApaLI...
!
1642      GTC GTG ACG CAG CCG CCC TCA GTG TCT GGG GCC CCA GGG CAG
      AGG GTC ACC ATC TCC TGC ACT GGG AGC AGC TCC AAC ATC GGG GCA
10 !
      BstEII...
1729      GGT TAT GAT GTA CAC TGG TAC CAG CAG CTT CCA GGA ACA GCC CCC AAA
1777      CTC CTC ATC TAT GGT AAC AGC AAT CGG CCC TCA GGG GTC CCT GAC CGA
1825      TTC TCT GGC TCC AAG TCT GGC ACC TCA GCC TCC CTG GCC ATC ACT
1870      GGG CTC CAG GCT GAG GAT GAG GCT GAT TAT
15 1900      TAC TGC CAG TCC TAT GAC AGC AGC CTG AGT
1930      GGC CTT TAT GTC TTC GGA ACT GGG ACC AAG GTC ACC GTC
!
!                                     BstEII...
1969      CTA GGT CAG CCC AAG GCC AAC CCC ACT GTC ACT
2002      CTG TTC CCG CCC TCC TCT GAG GAG CTC CAA GCC AAC AAG GCC ACA CTA
20 2050      GTG TGT CTG ATC AGT GAC TTC TAC CCG GGA GCT GTG ACA GTG GCC TGG
2098      AAG GCA GAT AGC AGC CCC GTC AAG GCG GGA GTG GAG ACC ACC ACA CCC
2146      TCC AAA CAA AGC AAC AAC AAG TAC GCG GCC AGC AGC TAT CTG AGC CTG
2194      ACG CCT GAG CAG TGG AAG TCC CAC AGA AGC TAC AGC TGC CAG GTC ACG
2242      CAT GAA GGG AGC ACC GTG GAG AAG ACA GTG GCC CCT ACA GAA TGT TCA
25 2290      TAA TAA ACCG CCTCCACCGG GCGCGCCAAT TCTATTTCAA GGAGACAGTC ATA
!
!                                     AscI.....
!
!
!           PelB signal----->
!           M   K   Y   L   L   P   T   A   A   A   G   L   L   L   L
30 2343      ATG AAA TAC CTA TTG CCT ACG GCA GCC GCT GGA TTG TTA TTA CTC
!
!           16  17  18  19  20          21  22
!           A   A   Q   P   A          M   A
!           2388      gcG GCC cag ccG GCC atg gcc
35 !
!           SfiI.....
!
!           NgoMI... (1/2)
!
!           NcoI.....
!

```



```

!                                     FR1 (DP47/V3-23) -----
!                                     23 24 25 26 27 28 29 30
!                                     E  V  Q  L  L  E  S  G
2409                                gaa|ggt|CAA|TTG|tta|gag|tct|ggt|
5  !                                     | MfeI  |
!
! -----FR1-----
!      31 32 33 34 35 36 37 38 39 40 41 42 43 44 45
!      G  G  L  V  Q  P  G  G  S  L  R  L  S  C  A
10 2433 |ggc|ggt|ctt|ggt|cag|cct|ggt|ggt|tct|tta|cgt|ctt|tct|tgc|gct|
!
! ----FR1----->|...CDR1.....|----FR2-----
!      46 47 48 49 50 51 52 53 54 55 56 57 58 59 60
!      A  S  G  F  T  F  S  S  Y  A  M  S  W  V  R
15 2478 |gct|TCC|GGA|ttc|act|ttc|tct|tCG|TAC|Gct|atg|tct|tgg|ggt|cgC|
!      | BspEI  |                | BsiWI  |                | BstXI.
!
! -----FR2----->|...CDR2.....
!      61 62 63 64 65 66 67 68 69 70 71 72 73 74 75
20  !      Q  A  P  G  K  G  L  E  W  V  S  A  I  S  G
2523 |CAa|gct|ccT|GGt|aaa|ggt|ttg|gag|tgg|ggt|tct|gct|atc|tct|ggt|
!      ...BstXI      |
!
! .....CDR2.....|----FR3----
25  !      76 77 78 79 80 81 82 83 84 85 86 87 88 89 90
!      S  G  G  S  T  Y  Y  A  D  S  V  K  G  R  F
2568 |tct|ggt|ggc|agt|act|tac|tat|gct|gac|tcc|ggt|aaa|ggt|cgc|ttc|
!
! -----FR3-----
!      91 92 93 94 95 96 97 98 99 100 101 102 103 104 105
!      T  I  S  R  D  N  S  K  N  T  L  Y  L  Q  M
2613 |act|atc|TCT|AGA|gac|aac|tct|aag|aat|act|ctc|tac|ttg|cag|atg|
!      | XbaI  |
35  !
! -----FR3----->|
!      106 107 108 109 110 111 112 113 114 115 116 117 118 119 120
!      N  S  L  R  A  E  D  T  A  V  Y  Y  C  A  K
2658 |aac|agC|TTA|AGg|gct|gag|gac|act|GCA|Gtc|tac|tat|tgc|gct|aaa|

```

```

!           |AflIII |           | PstI |
!
!           .....CDR3.....|----FR4-----
!           121 122 123 124 125 126 127 128 129 130 131 132 133 134 135
5 !           D   Y   E   G   T   G   Y   A   F   D   I   W   G   Q   G
2703 |gac|tat|gaa|ggt|act|ggt|tat|gct|ttc|gaC|ATA|TGg|ggt|caa|ggt|
!                                     | NdeI |(1/4)
!
!           -----FR4----->|
10 !           136 137 138 139 140 141 142
!           T   M   V   T   V   S   S
2748 |act|atG|GTC|ACC|gtc|tct|agt
!           | BstEII |
! From BstEII onwards, pV323 is same as pCES1, except as noted.
15 ! BstEII sites may occur in light chains; not likely to be unique in final
! vector.
!
!           143 144 145 146 147 148 149 150 151 152
!           A   S   T   K   G   P   S   V   F   P
20 2769 gcc tcc acc aaG GGC CCa tcg GTC TTC ccc
!           Bsp120I.      BbsI...(2/2)
!           ApaI....
!
!           153 154 155 156 157 158 159 160 161 162 163 164 165 166 167
25 !           L   A   P   S   S   K   S   T   S   G   G   T   A   A   L
2799 ctg gca ccC TCC TCc aag agc acc tct ggg ggc aca gcg gcc ctg
!           BseRI...(2/2)
!
!           168 169 170 171 172 173 174 175 176 177 178 179 180 181 182
30 !           G   C   L   V   K   D   Y   F   P   E   P   V   T   V   S
2844 ggc tgc ctg GTC AAG GAC TAC TTC CCc gaA CCG GTg acg gtg tcg
!           AgeI....
!
!           183 184 185 186 187 188 189 190 191 192 193 194 195 196 197
35 !           W   N   S   G   A   L   T   S   G   V   H   T   F   P   A
2889 tgg aac tca GGC GCC ctg acc agc ggc gtc cac acc ttc ccg gct
!           KasI...(1/4)
!
!           198 199 200 201 202 203 204 205 206 207 208 209 210 211 212

```

```

!       V   L   Q   S   S   G   L   Y   S   L   S   S   V   V   T
2934   gtc cta cag tCt agc GGa ctc tac tcc ctc agc agc gta gtg acc
!       (Bsu36I...) (knocked out)
!
5  !       213 214 215 216 217 218 219 220 221 222 223 224 225 226 227
!       V   P   S   S   S   L   G   T   Q   T   Y   I   C   N   V
2979   gtg ccC tCt tct agc tTG Ggc acc cag acc tac atc tgc aac gtg
!       (BstXI.....)N.B. destruction of BstXI & BpmI sites.
!
10 !       228 229 230 231 232 233 234 235 236 237 238 239 240 241 242
!       N   H   K   P   S   N   T   K   V   D   K   K   V   E   P
3024   aat cac aag ccc agc aac acc aag gtg gac aag aaa gtt gag ccc
!
!       243 244 245
15 !       K   S   C   A   A   A   H   H   H   H   H   H   S   A
3069   aaa tct tgt GCG GCC GcT cat cac cac cat cat cac tct gct
!       NotI.....
!
!       E   Q   K   L   I   S   E   E   D   L   N   G   A   A
20 3111   gaa caa aaa ctc atc tca gaa gag gat ctg aat ggt gcc gca
!
!
!       D   I   N   D   D   R   M   A   S   G   A
3153   GAT ATC aac gat gat cgt atg   gct AGC   ggc gcc
25 !       rEK cleavage site.....   NheI...   KasI...
!       EcoRV..
!
! Domain 1 -----
!       A   E   T   V   E   S   C   L   A
30 3183   gct gaa act gtt gaa agt tgt tta gca
!
!
!       K   P   H   T   E   I   S   F
3210   aaa ccc cat aca gaa aat tca ttt
35 !
!       T   N   V   W   K   D   D   K   T
3234   aCT AAC GTC TGG AAA GAC GAC AAA ACT
!
!       L   D   R   Y   A   N   Y   E   G   C   L   W   N   A   T   G   V

```

```

3261 tta gat cgt tac gct aac tat gag ggt tgt ctg tgG AAT GcT aca ggc gtt
!                                     BsmI_____
!
!       V   V   C   T   G   D   E   T   Q   C   Y   G   T   W   V   P   I
5  3312 gta gtt tgt act ggt GAC GAA ACT CAG TGT TAC GGT ACA TGG GTT cct att
!
!       G   L   A   I   P   E   N
3363 ggg ctt gct atc cct gaa aat
!
10 ! L1 linker -----
!       E   G   G   G   S   E   G   G   G   S
3384 gag ggt ggt ggc tct gag ggt ggc ggt tct
!
!       E   G   G   G   S   E   G   G   G   T
15 3414 gag ggt ggc ggt tct gag ggt ggc ggt act
!
!   Domain 2 -----
3444 aaa cct cct gag tac ggt gat aca cct att ccg ggc tat act tat atc aac
3495 cct ctg gac ggc act tat ccg cct ggt act gag caa aac ccc gct aat cct
20 3546 aat cct tct ctt GAG GAG tct cag cct ctt aat act ttc atg ttt cag aat
!
!                                     BseRI_____
3597 aat agg ttc cga aat agg cag ggg gca tta act gtt tat acg ggc act
3645 gtt act caa ggc act gac ccc gtt aaa act tat tac cag tac act cct
3693 gta tca tca aaa gcc atg tat gac gct tac tgg aac ggt aaa ttC AGA
25 !                                     AlwNI
3741 GAC TGc gct ttc cat tct ggc ttt aat gaa gat cca ttc gtt tgt gaa
!       AlwNI
3789 tat caa ggc caa tcg tct gac ctg cct caa cct cct gtc aat gct
!
30 3834 ggc ggc ggc tct
!   start L2 -----
3846 ggt ggt ggt tct
3858 ggt ggc ggc tct
3870 gag ggt ggt ggc tct gag ggt ggc ggt tct
35 3900 gag ggt ggc ggc tct gag gga ggc ggt tcc
3930 ggt ggt ggc tct ggt      ! end L2
!
!   Domain 3 -----
!       S   G   D   F   D   Y   E   K   M   A   N   A   N   K   G   A

```

3945 tcc ggt gat ttt gat tat gaa aag atg gca aac gct aat aag ggg gct
!
! M T E N A D E N A L Q S D A K G
3993 atg acc gaa aat gcc gat gaa aac gcg cta cag tct gac gct aaa ggc
5 !
! K L D S V A T D Y G A A I D G F
4041 aaa ctt gat tct gtc gct act gat tac ggt gct gct atc gat ggt_ttc
!
! I G D V S G L A N G N G A T G D
10 4089 att ggt gac gtt tcc ggc ctt gct aat ggt aat ggt gct act ggt gat
!
! F A G S N S Q M A Q V G D G D N
4137 ttt gct ggc tct aat tcc caa atg gct caa gtc ggt gac ggt gat aat
!
15 ! S P L M N N F R Q Y L P S L P Q
4185 tca cct tta atg aat aat ttc cgt caa tat tta cct tcc ctc cct caa
!
! S V E C R P F V F S A G K P Y E
20 4233 tcg gtt gaa tgt cgc cct ttt gtc ttt agc gct ggt aaa cca tat gaa
!
! F S I D C D K I N L F R
4281 ttt tct att gat tgt gac aaa ata aac tta ttc cgt
!
! End Domain 3
!
25 ! G V F A F L L Y V A T F M Y V F140
4317 ggt gtc ttt gcg ttt ctt tta tat gtt gcc acc ttt atg tat gta ttt
!
! start transmembrane segment
!
! S T F A N I L
30 4365 tct acg ttt gct aac ata ctg
!
! R N K E S
4386 cgt aat aag gag tct TAA ! stop of iii
!
! Intracellular anchor.
35 !
! M1 P2 V L L5 G I P L L10 L R F L G15
4404 tc ATG cca gtt ctt ttg ggt att ccg tta tta ttg cgt ttc ctc ggt
!
! Start VI
!

4451 ttc ctt ctg gta act ttg ttc ggc tat ctg ctt act ttt ctt aaa aag
4499 ggc ttc ggt aag ata gct att gct att tca ttg ttt ctt gct ctt att
4547 att ggg ctt aac tca att ctt gtg ggt tat ctc tct gat att agc gct
4595 caa tta ccc tct gac ttt gtt cag ggt gtt cag tta att ctc ccg tct
5 4643 aat gcg ctt ccc tgt ttt tat gtt att ctc tct gta aag gct gct att
4691 ttc att ttt gac gtt aaa caa aaa atc gtt tct tat ttg gat tgg gat
!
! M1 A2 V3 F5 L10 G13
4739 aaa TAA t ATG gct gtt tat ttt gta act ggc aaa tta ggc tct gga
10 ! end VI Start gene I
!
! 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28
! K T L V S V G K I Q D K I V A
4785 aag acg ctc gtt agc gtt ggt aag att cag gat aaa att gta gct
15 !
! 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43
! G C K I A T N L D L R L Q N L
4830 ggg tgc aaa ata gca act aat ctt gat tta agg ctt caa aac ctc
!
20 ! 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58
! P Q V G R F A K T P R V L R I
4875 ccg caa gtc ggg agg ttc gct aaa acg cct cgc gtt ctt aga ata
!
! 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73
25 ! P D K P S I S D L L A I G R G
4920 ccg gat aag cct tct ata tct gat ttg ctt gct att ggg cgc ggt
!
! 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88
! N D S Y D E N K N G L L V L D
30 4965 aat gat tcc tac gat gaa aat aaa aac ggc ttg ctt gtt ctc gat
!
! 89 90 91 92 93 94 95 96 97 98 99 100 101 102 103
! E C G T W F N T R S W N D K E
5010 gag tgc ggt act tgg ttt aat acc cgt tct tgg aat gat aag gaa
35 !
! 104 105 106 107 108 109 110 111 112 113 114 115 116 117 118
! R Q P I I D W F L H A R K L G
5055 aga cag ccg att att gat tgg ttt cta cat gct cgt aaa tta gga
!

! 119 120 121 122 123 124 125 126 127 128 129 130 131 132 133
! W D I I F L V Q D L S I V D K
5100 tgg gat att att ttt ctt gtt cag gac tta tct att gtt gat aaa
!
5 ! 134 135 136 137 138 139 140 141 142 143 144 145 146 147 148
! Q A R S A L A E H V V Y C R R
5145 cag gcg cgt tct gca tta gct gaa cat gtt gtt tat tgt cgt cgt
!
! 149 150 151 152 153 154 155 156 157 158 159 160 161 162 163
10 ! L D R I T L P F V G T L Y S L
5190 ctg gac aga att act tta cct ttt gtc ggt act tta tat tct ctt
!
! 164 165 166 167 168 169 170 171 172 173 174 175 176 177 178
! I T G S K M P L P K L H V G V
15 5235 att act ggc tcg aaa atg cct ctg cct aaa tta cat gtt ggc gtt
!
! 179 180 181 182 183 184 185 186 187 188 189 190 191 192 193
! V K Y G D S Q L S P T V E R W
5280 gtt aaa tat ggc gat tct caa tta agc cct act gtt gag cgt tgg
20 !
! 194 195 196 197 198 199 200 201 202 203 204 205 206 207 208
! L Y T G K N L Y N A Y D T K Q
5325 ctt tat act ggt aag aat ttg tat aac gca tat gat act aaa cag
!
25 ! 209 210 211 212 213 214 215 216 217 218 219 220 221 222 223
! A F S S N Y D S G V Y S Y L T
5370 gct ttt tct agt aat tat gat tcc ggt gtt tat tct tat tta acg
!
! 224 225 226 227 228 229 230 231 232 233 234 235 236 237 238
30 ! P Y L S H G R Y F K P L N L G
5415 cct tat tta tca cac ggt cgg tat ttc aaa cca tta aat tta ggt
!
! 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253
! Q K M K L T K I Y L K K F S R
35 5460 cag aag atg aaa tta act aaa ata tat ttg aaa aag ttt tct cgc
!
! 254 255 256 257 258 259 260 261 262 263 264 265 266 267 268
! V L C L A I G F A S A F T Y S
5505 gtt ctt tgt ctt gcg att gga ttt gca tca gca ttt aca tat agt

```

!
!      269 270 271 272 273 274 275 276 277 278 279 280 281 282 283
!      Y   I   T   Q   P   K   P   E   V   K   K   V   V   S   Q
5550 tat ata acc caa cct aag ccg gag gtt aaa aag gta gtc tct cag
5  !
!      284 285 286 287 288 289 290 291 292 293 294 295 296 297 298
!      T   Y   D   F   D   K   F   T   I   D   S   S   Q   R   L
5595 acc tat gat ttt gat aaa ttc act att gac tct tct cag cgt ctt
!
10 !      299 300 301 302 303 304 305 306 307 308 309 310 311 312 313
!      N   L   S   Y   R   Y   V   F   K   D   S   K   G   K   L
5640 aat cta agc tat cgc tat gtt ttc aag gat tct aag gga aaa TTA
!
!
!
!
15 !      314 315 316 317 318 319 320 321 322 323 324 325 326 327 328
!      I   N   S   D   D   L   Q   K   Q   G   Y   S   L   T   Y
5685 ATT AAt agc gac gat tta cag aag caa ggt tat tca ctc aca tat
!
!
!
!
20 !      329 330 331 332 333 334 335 336 337 338 339 340 341 342 343
!      i   I   D   L   C   T   V   S   I   K   K   G   N   S   N   E
!      iv
!
5730 att gat tta tgt act gtt tcc att aaa aaa ggt aat tca aAT Gaa
!
!
!
!
25 !
!
!      344 345 346 347 348 349
!      i   I   V   K   C   N   .End of I
!      iv   L3 L   N5 V   I7 N   F   V10
5775 att gtt aaa tgt aat TAA T TTT GTT
30 ! IV continued.....
5800 ttc ttg atg ttt gtt tca tca tct tct ttt gct cag gta att gaa atg
5848 aat aat tcg cct ctg cgc gat ttt gta act tgg tat tca aag caa tca
5896 ggc gaa tcc gtt att gtt tct ccc gat gta aaa ggt act gtt act gta
5944 tat tca tct gac gtt aaa cct gaa aat cta cgc aat ttc ttt att tct
35 5992 gtt tta cgt gct aat aat ttt gat atg gtt ggt tca att cct tcc ata
6040 att cag aag tat aat cca aac aat cag gat tat att gat gaa ttg cca
6088 tca tct gat aat cag gaa tat gat gat aat tcc gct cct tct ggt ggt
6136 ttc ttt gtt ccg caa aat gat aat gtt act caa act ttt aaa att aat
6184 aac gtt ccg gca aag gat tta ata cga gtt gtc gaa ttg ttt gta aag

```


6232 tct aat act tct aaa tcc tca aat gta tta tct att gac ggc tct aat
6280 cta tta gtt gtt TCT gca cct aaa gat att tta gat aac ctt cct caa

! ApaLI removed

5 6328 ttc ctt tct act gtt gat ttg cca act gac cag ata ttg att gag ggt
6376 ttg ata ttt gag gtt cag caa ggt gat gct tta gat ttt tca ttt gct
6424 gct ggc tct cag cgt ggc act gtt gca ggc ggt gtt aat act gac cgc
6472 ctc acc tct gtt tta tct tct gct ggt ggt tgc ttc ggt att ttt aat
6520 ggc gat gtt tta ggg cta tca gtt cgc gca tta aag act aat agc cat
6568 tca aaa ata ttg tct gtg cca cgt att ctt acg ctt tca ggt cag aag
10 6616 ggt tct atc tct gtT GGC CAg aat gtc cct ttt att act ggt cgt gtg

! MscI _____

6664 act ggt gaa tct gcc aat gta aat aat cca ttt cag acg att gag cgt
6712 caa aat gta ggt att tcc atg agc gtt ttt cct gtt gca atg gct ggc
6760 ggt aat att gtt ctg gat att acc agc aag gcc gat agt ttg agt tct
15 6808 tct act cag gca agt gat gtt att act aat caa aga agt att gct aca
6856 acg gtt aat ttg cgt gat gga cag act ctt tta ctc ggt ggc ctc act
6904 gat tat aaa aac act tct caa gat tct ggc gta ccg ttc ctg tct aaa
6952 atc cct tta atc ggc ctc ctg ttt agc tcc cgc tct gat tcc aac gag
7000 gaa agc acg tta tac gtg ctc gtc aaa gca acc ata gta cgc gcc ctg
20 7048 TAG cggcgcatt

! End IV

7060 aagcgcggcg ggtgtggtgg ttacgcgcag cgtgaccgct acacttgcca gcgccttagc
7120 gcccgctcct ttcgctttct tcccttcctt tctcgccacg ttcGCCGGCt ttccccgtca

! NgoMI _____

25 7180 agctctaaat cgggggctcc ctttaggggtt ccgatttagt gctttacggc acctcgacct
7240 caaaaaactt gatttggttg atggttCACG TAGTGggcca tcgccctgat agacgggtttt

! DraIII _____

7300 tcgccctttG ACGTTGGAGT Ccacgttctt taatagtga ctcttggtcc aaactggaac

! DrdI _____

30 7360 aacactcaac cctatctcgg gctattcttt tgatttataa gggattttgc cgatttcgga
7420 accaccatca aacaggattt tcgcctgctg gggcaaacca gcgtggaccg cttgctgcaa
7480 ctctctcagg gccaggcggg gaagggaat CAGCTGttgc cCGTCTCact ggtgaaaaga

! PvuII. BsmBI.

7540 aaaaccaccc tGGATCC AAGCTT

35 ! BamHI HindIII (1/2)

! Insert carrying bla gene

7563 gcagggtg gcacttttcg gggaaatgtg cgcggaaccc

7600 ctatttggtt atttttctaa atacattcaa atatGTATCC gctcatgaga caataaccct

! BciVI

MISSING AT THE TIME OF PUBLICATION

8790 CCTGAGG
! Bsu36I_
8797 ccgat actgtcgtcg tccctcaaa ctggcagatg
8832 cacggttacg atgcgcccat ctacaccaac gtaacctatc ccattacggt caatccgccg
5 8892 tttgttccca cggagaatcc gacgggttgt tactcgtcga catttaattgt tgatgaaagc
8952 tggctacagg aaggccagac gcgaattatt tttgatggcg ttcctattgg ttaaaaaatg
9012 agctgattta acaaaaattt aacgcgaatt ttaacaaaat attaacgttt acaATTAA
! SwaI...
9072 Tatttgctta tacaatcttc ctgttttttg ggcttttctg attatcaacc GGGGTACat
10 ! RBS?
9131 ATG att gac atg cta gtt tta cga tta ccg ttc atc gat tct ctt gtt tgc
! Start gene II
9182 tcc aga ctc tca ggc aat gac ctg ata gcc ttt gtA GAT CTc tca aaa ata
! BglII...
15 9233 gct acc ctc tcc ggc atg aat tta tca gct aga acg gtt gaa tat cat att
9284 gat ggt gat ttg act gtc tcc ggc ctt tct cac cct ttt gaa tct tta cct
9335 aca cat tac tca ggc att gca ttt aaa ata tat gag ggt tct aaa aat ttt
9386 tat cct tgc gtt gaa ata aag gct tct ccc gca aaa gta tta cag ggt cat
9437 aat gtt ttt ggt aca acc gat tta gct tta tgc tct gag gct tta ttg ctt
20 9488 aat ttt gct aat tct ttg cct tgc ctg tat gat tta ttg gat gtt ! 9532
! gene II continues

Table 120B: Sequence of MALIA3, condensed

LOCUS	MALIA3	9532	CIRCULAR
ORIGIN			
	1	AATGCTACTA CTATTAGTAG AATTGATGCC ACCTTTTCAG CTCGCGCCCC AAATGAAAAT	
5	61	ATAGCTAAAC AGGTTATTGA CCATTTGCGA AATGTATCTA ATGGTCAAAC TAAATCTACT	
	121	CGTTCGCAGA ATTGGGAATC AACTGTTACA TGGAATGAAA CTTCCAGACA CCGTACTTTA	
	181	GTTGCATATT TAAAACATGT TGAGCTACAG CACCAGATTC AGCAATTAAG CTCTAAGCCA	
	241	TCCGCAAAAA TGACCTCTTA TCAAAAGGAG CAATTAAAGG TACTCTCTAA TCCTGACCTG	
	301	TTGGAGTTTG CTTCGGTCT GGTTCGCTTT GAAGCTCGAA TTAAACGCG ATATTTGAAG	
10	361	TCTTTCGGGC TTCCTCTTAA TCTTTTGGAT GCAATCCGCT TTGCTTCTGA CTATAATAGT	
	421	CAGGGTAAAG ACCTGATTTT TGATTTATGG TCATTCTCGT TTTCTGAACT GTTTAAAGCA	
	481	TTTGAGGGGG ATTCAATGAA TATTTATGAC GATTCCGCAG TATTGGACGC TATCCAGTCT	
	541	AAACATTTTA CTATTACCCC CTCTGGCAAA ACTTCTTTTG CAAAAGCCTC TCGCTATTTT	
	601	GGTTTTTATC GTCGTCTGGT AAACGAGGGT TATGATAGTG TTGCTCTTAC TATGCCTCGT	
15	661	AATTCCTTTT GGCGTTATGT ATCTGCATTA GTTGAATGTG GTATTCCTAA ATCTCAACTG	
	721	ATGAATCTTT CTACCTGTAA TAATGTTGTT CCGTTAGTTC GTTTTATTAA CGTAGATTTT	
	781	TCTTCCCAAC GTCCTGACTG GTATAATGAG CCAGTTCTTA AAATCGCATA AGGTAATTCA	
	841	CAATGATTAA AGTTGAAATT AAACCATCTC AAGCCCAATT TACTACTCGT TCTGGTGTTT	
	901	CTCGTCAGGG CAAGCCTTAT TCACTGAATG AGCAGCTTTG TTACGTTGAT TTGGGTAATG	
20	961	AATATCCGGT TCTTGTC AAG ATTACTCTTG ATGAAGGTCA GCCAGCCTAT GCGCCTGGTC	
	1021	TGTACACCGT TCATCTGTCC TCTTTC AAG TTGGTCAGTT CGGTTCCTT ATGATTGACC	
	1081	GTCTGCGCCT CGTTCGGCT AAGTAACATG GAGCAGGTCG CGGATTCGA CACAATTTAT	
	1141	CAGGCGATGA TACAAATCTC CGTTGTACTT TGTTTCGCGC TTGGTATAAT CGCTGGGGGT	
	1201	CAAAGATGAG TGTTTTAGTG TATTCCTTCG CCTCTTTCGT TTTAGGTTGG TGCCTTCGTA	
25	1261	GTGGCATTAC GTATTTTACC CGTTTAAATG AAACCTTCCTC ATGAAAAAGT CTTTAGTCCT	
	1321	CAAAGCCTCT GTAGCCGTTG CTACCCTCGT TCCGATGCTG TCTTTCGCTG CTGAGGGTGA	
	1381	CGATCCCGCA AAAGCGGCCT TTAACCTCCT GCAAGCCTCA GCGACCGAAT ATATCGGTTA	
	1441	TGCGTGCGCG ATGGTTGTTG TCATTGTCGG CGCAACTATC GGTATCAAGC TGTTTAAGAA	
	1501	ATTACCTCG AAAGCAAGCT GATAAACCGA TACAATTAAA GGCTCCTTTT GGAGCCTTTT	
30	1561	TTTTTGAGAG TTTTCAACGT GAAAAATTA TTATTCGCAA TTCCTTTAGT TGTTCCTTTC	
	1621	TATTCTCACA GTGCACAGTC TGTCGTGACG CAGCCGCCCT CAGTGTCTGG GGCCCCAGGG	
	1681	CAGAGGGTCA CCATCTCCTG CACTGGGAGC AGCTCCAACA TCGGGGCAGG TTATGATGTA	
	1741	CACTGGTACC AGCAGCTTCC AGGAACAGCC CCCAACTCC TCATCTATGG TAACAGCAAT	
	1801	CGGCCCTCAG GGTCCCTGA CCGATTCTCT GGCTCCAAGT CTGGCACCTC AGCCTCCCTG	
35	1861	GCCATCACTG GGCTCCAGGC TGAGGATGAG GCTGATTATT ACTGCCAGTC CTATGACAGC	
	1921	AGCCTGAGTG GCCTTTATGT CTTCGGAAC TGGGACCAAG TCACCGTCCT AGGTCAGCCC	
	1981	AAGGCCAACC CCACTGTCAC TCTGTTCCCG CCCTCCTCTG AGGAGCTCCA AGCCAACAAG	
	2041	GCCACACTAG TGTGTCTGAT CAGTGACTTC TACCCGGGAG CTGTGACAGT GGCCTGGAAG	
	2101	GCAGATAGCA GCCCCGTCAA GGCGGGAGTG GAGACCACCA CACCCTCCAA ACAAAGCAAC	

2161 AACAAAGTACG CGGCCAGCAG CTATCTGAGC CTGACGCCTG AGCAGTGGAA GTCCACAGA
2221 AGCTACAGCT GCCAGGTCAC GCATGAAGGG AGCACCCTGG AGAAGACAGT GGCCCTACA
2281 GAATGTTTCAT AATAAACCGC CTCCACCGGG CGCGCCAATT CTATTTCAAG GAGACAGTCA
2341 TAATGAAATA CCTATTGCCT ACGGCAGCCG CTGGATTGTT ATTACTCGCG GCCCAGCCGG
5 2401 CCATGGCCGA AGTTCAATTG TTAGAGTCTG GTGGCGGTCT TGTTCAGCCT GGTGGTTCTT
2461 TACGTCTTTC TTGCGCTGCT TCCGGATTCA CTTTCTCTTC GTACGCTATG TCTTGGGTTTC
2521 GCCAAGCTCC TGGTAAAGGT TTGGAGTGGG TTTCTGCTAT CTCTGGTTCT GGTGGCAGTA
2581 CTTACTATGC TGA CTCCGTT AAAGGTCGCT TCACTATCTC TAGAGACAAC TCTAAGAATA
2641 CTCTCTACTT GCAGATGAAC AGCTTAAGGG CTGAGGACAC TGCAGTCTAC TATTGCGCTA
10 2701 AAGACTATGA AGGTACTGGT TATGCTTTCG ACATATGGGG TCAAGGTACT ATGGTCACCG
2761 TCTCTAGTGC CTCCACCAAG GGCCCATCGG TCTTCCCCCT GGCACCCCTCC TCCAAGAGCA
2821 CCTCTGGGGG CACAGCGGCC CTGGGCTGCC TGGTCAAGGA CTACTTCCCC GAACCGGTGA
2881 CGGTGTCGTG GAACTCAGGC GCCCTGACCA GCGGCGTCCA CACCTTCCCG GCTGTCCTAC
2941 AGTCTAGCGG ACTCTACTCC CTCAGCAGCG TAGTGACCGT GCCCTCTTCT AGCTTGGGCA
15 3001 CCCAGACCTA CATCTGCAAC GTGAATCACA AGCCCAGCAA CACCAAGGTG GACAAGAAAG
3061 TTGAGCCCAA ATCTTGTCG GCGGCTCATC ACCACCATCA TCACTCTGCT GAACAAAAC
3121 TCATCTCAGA AGAGGATCTG AATGGTGCCG CAGATATCAA CGATGATCGT ATGGCTGGCG
3181 CCGCTGAAAC TGTGAAAGT TGTTTAGCAA AACCCATAC AGAAAATTCA TTTACTAACG
3241 TCTGGAAGA CGACAAAAC TTAGATCGTT ACGCTAACTA TGAGGGTTGT CTGTGGAATG
20 3301 CTACAGGCGT TGTAGTTTGT ACTGGTGACG AAACCTAGTG TTACGGTACA TGGGTTCTTA
3361 TTGGGCTTGC TATCCCTGAA AATGAGGGTG GTGGCTCTGA GGGTGGCGGT TCTGAGGGTG
3421 GCGGTTCTGA GGGTGGCGGT ACTAAACCTC CTGAGTACGG TGATACACCT ATTCCGGGCT
3481 ATACTTATAT CAACCTCTC GACGGCACTT ATCCGCTGG TACTGAGCAA AACCCGCTA
3541 ATCCTAATCC TTCTCTTGAG GAGTCTCAGC CTCTTAATAC TTTCATGTTT CAGAATAATA
25 3601 GGTTCCGAAA TAGGCAGGGG GCATTAAC TGTTATACGG CACTGTTACT CAAGGCACTG
3661 ACCCGTTTAA AACTTATTAC CAGTACACTC CTGTATCATC AAAAGCCATG TATGACGCTT
3721 ACTGGAACGG TAAATTCAGA GACTGCGCTT TCCATTCTGG CTTTAATGAA GATCCATTCTG
3781 TTTGTGAATA TCAAGGCCAA TCGTCTGACC TGCCTCAACC TCCTGTCAAT GCTGGCGGCG
3841 GCTCTGGTGG TGGTCTGGT GGCGGCTCTG AGGGTGGTGG CTCTGAGGGT GCGGTTCTG
30 3901 AGGGTGGCGG CTCTGAGGGA GGCGGTTCG GTGGTGGCTC TGGTTCCGGT GATTTTGATT
3961 ATGAAAAGAT GGCAAACGCT AATAAGGGG CTATGACCGA AAATGCCGAT GAAAACGCGC
4021 TACAGTCTGA CGCTAAAGGC AAACCTGATT CTGTCGCTAC TGATTACGGT GCTGCTATCG
4081 ATGGTTTCAT TGGTGACGTT TCCGGCCTTG CTAATGGTAA TGGTGCTACT GGTGATTTTG
4141 CTGGCTCTAA TTCCCAAATG GCTCAAGTCG GTGACGGTGA TAATTCACCT TTAATGAATA
35 4201 ATTTCCGTCA ATATTTACCT TCCCTCCCTC AATCGGTTGA ATGTCGCCCT TTTGTCTTTA
4261 GCGCTGGTAA ACCATATGAA TTTTCTATTG ATTGTGACAA AATAAACTTA TTCCGTGGTG
4321 TCTTTGCGTT TCTTTTATAT GTTGCCACCT TTATGTATGT ATTTTCTACG TTTGCTAACA
4381 TACTGCGTAA TAAGGAGTCT TAATCATGCC AGTTCTTTTG GGTATTCCGT TATTATTGCG
4441 TTTCCTCGGT TTCCTTCTGG TAACTTTGTT CGGCTATCTG CTTACTTTTC TTAAAAAGGG

5 4501 CTTTCGGTAAG ATAGCTATTG CTATTTTCATT GTTTCCTTGCT CTTATTATTG GGCTTAACTC
4561 AATTCTTGTG GGTATCTCT CTGATATTAG CGCTCAATTA CCCTCTGACT TTGTTTCAGGG
4621 TGTTCAAGTA ATTCTCCCGT CTAATGCGCT TCCCTGTTTT TATGTTATTC TCTCTGTAAA
4681 GGCTGCTATT TTCATTTTTG ACGTTAAACA AAAAATCGTT TCTTATTTGG ATTGGGATAA
10 4741 ATAATATGGC TGTTTATTTT GTAAGTGGCA AATTAGGCTC TGGAAAGACG CTCGTTAGCG
4801 TTGGTAAGAT TCAGGATAAA ATTGTAGCTG GGTGCAAAAT AGCAACTAAT CTTGATTTAA
4861 GGCTTCAAAA CCTCCCGCAA GTCGGGAGGT TCGCTAAAC GCCTCGCGTT CTTAGAATAC
4921 CGGATAAGCC TTCTATATCT GATTTGCTTG CTATTGGGCG CGGTAATGAT TCCTACGATG
4981 AAAATAAAAA CGGCTTGCTT GTTCTCGATG AGTGCGGTAC TTGGTTTAAAT ACCCGTTCTT
15 5041 GGAATGATAA GGAAAGACAG CCGATTATTG ATTGGTTTCT ACATGCTCGT AAATTAGGAT
5101 GGGATATTAT TTTTCTTGTT CAGGACTTAT CTATTGTTGA TAAACAGGCG CGTTCTGCAT
5161 TAGCTGAACA TGTTGTTTAT TGTCGTCGTC TGGACAGAAT TACTTTACCT TTTGTCGGTA
5221 CTTTATATTC TCTTATTACT GGCTCGAAAA TGCCTCTGCC TAAATTACAT GTTGGCGTTG
5281 TTAAATATGG CGATTCTCAA TTAAGCCCTA CTGTTGAGCG TTGGCTTTAT ACTGGTAAGA
20 5341 ATTTGTATAA CGCATATGAT ACTAAACAGG CTTTTTCTAG TAATTATGAT TCCGGTGTTT
5401 ATTCTTATTT AACGCCCTAT TTATCACACG GTCGGTATTT CAAACCATTA AATTTAGGTC
5461 AGAAGATGAA ATTAAGTAAA ATATATTTGA AAAAGTTTTT TCGCGTTCTT TGTCTTGCGA
5521 TTGGATTTGC ATCAGCATTT ACATATAGTT ATATAACCCA ACCTAAGCCG GAGGTTAAAA
5581 AGGTAGTCTC TCAGACCTAT GATTTTGATA AATTCATAT TGACTCTTCT CAGCGTCTTA
25 5641 ATCTAAGCTA TCGCTATGTT TTCAAGGATT CTAAGGGAAA ATTAATTAAT AGCGACGATT
5701 TACAGAAGCA AGGTATTCA CTCACATATA TTGATTTATG TACTGTTTCC ATTAAAAAAG
5761 GTAATTCAAA TGAAATTGTT AAATGTAATT AATTTTGTTT TCTTGATGTT TGTTCATCA
5821 TCTTCTTTTG CTCAGGTAAT TGAAATGAAT AATTCGCCTC TCGCGGATTT TGTAAGTTGG
5881 TATTCAAAGC AATCAGGCGA ATCCGTTATT GTTCTCTCCG ATGTAAAAGG TACTGTTACT
30 5941 GTATATTCAT CTGACGTAA ACCTGAAAAT CTACGCAATT TCTTTATTTT TGTTTTACGT
6001 GCTAATAATT TTGATATGGT TGGTTCAATT CCTTCCATAA TTCAGAAGTA TAATCCAAAC
6061 AATCAGGATT ATATTGATGA ATTGCCATCA TCTGATAATC AGGAATATGA TGATAATTCC
6121 GCTCCTTCTG GTGGTTTCTT TGTTCCGCAA AATGATAATG TTAAGTCAAC TTTTAAATTT
6181 AATAACGTTT GGGCAAAGGA TTTAATACGA GTTGTGCAAT TGTGTTGAAA GTCTAATACT
35 6241 TCTAAATCCT CAAATGTATT ATCTATTGAC GGCTCTAATC TATTAGTTGT TTCTGCACCT
6301 AAAGATATTT TAGATAACCT TCCTCAATTC CTTTCTACTG TTGATTTGCC AACTGACCAG
6361 ATATTGATTG AGGGTTTGAT ATTTGAGGTT CAGCAAGGTG ATGCTTTAGA TTTTTCATTT
6421 GCTGCTGGCT CTCAGCGTGG CACTGTTGCA GGCGGTGTTA ATACTGACCG CCTCACCTCT
6481 GTTTTATCTT CTGCTGGTGG TTCGTTGCGT ATTTTAAATG GCGATGTTTT AGGGCTATCA
6541 GTTCGCGCAT TAAAGACTAA TAGCCATTCA AAAATATTGT CTGTGCCACG TATTCTTACG
6601 CTTTCAGGTC AGAAGGGTTC TATCTCTGTT GGCCAGAATG TCCCTTTTAT TACTGGTCGT
6661 GTGACTGGTG AATCTGCCAA TGTAATAAAT CCATTTGAGA CGATTGAGCG TCAAATGTA
6721 GGTATTTCCA TGAGCGTTTT TCCTGTTGCA ATGGCTGGCG GTAATATTGT TCTGGATATT
6781 ACCAGCAAGG CCGATAGTTT GAGTTCCTCT ACTCAGGCAA GTGATGTTAT TACTAATCAA

5 6841 AGAAGTATTG CTACAACGGT TAATTTGCGT GATGGACAGA CTCTTTTACT CGGTGGCCTC
6901 ACTGATTATA AAAAACAATC TCAAGATTCT GGCGTACCGT TCCTGTCTAA AATCCCTTTA
6961 ATCGGCCTCC TGTTTAGCTC CCGCTCTGAT TCCAACGAGG AAAGCACGTT ATACGTGCTC
7021 GTCAAAGCAA CCATAGTACG CGCCCTGTAG CGGCGCATTA AGCGCGGCGG GTGTGGTGGT
7081 TACGCGCAGC GTGACCGCTA CACTTGCCAG CGCCCTAGCG CCCGCTCCTT TCGCTTTCTT
7141 CCCTTCCTTT CTCGCCACGT TCGCCGGCTT TCCCCGTCAA GCTCTAAATC GGGGGCTCCC
7201 TTTAGGGTTC CGATTTAGTG CTTTACGGCA CCTCGACCCC AAAAAACTTG ATTTGGGTGA
7261 TGGTTCACGT AGTGGGCCAT CGCCCTGATA GACGGTTTTT CGCCTTTTGA CGTTGGAGTC
10 7321 CACGTTCTTT AATAGTGGAC TCTTGTTCCA AACTGGAACA AACTCAACC CTATCTCGGG
7381 CTATTCTTTT GATTTATAAG GGATTTTGCC GATTTTCGGA CCACCATCAA ACAGGATTTT
7441 CGCCTGCTGG GGCAAACCAG CGTGGACCGC TTGCTGCAAC TCTCTCAGGG CCAGGCGGTG
7501 AAGGGCAATC AGCTGTTGCC CGTCTCACTG GTGAAAAGAA AAACCACCCT GGATCCAAGC
7561 TTGCAGGTGG CACTTTTCGG GGAAATGTGC GCGGAACCCC TATTTGTTTA TTTTCTAAA
7621 TACATTCAAA TATGTATCCG CTCATGAGAC AATAACCCTG ATAAATGCTT CAATAATATT
15 7681 GAAAAAGGAA GAGTATGAGT ATTCAACATT TCCGTGTCGC CTTATTCCC TTTTTGCGG
7741 CATTTTGCCT TCCTGTTTTT GCTCACCCAG AAACGCTGGT GAAAGTAAA GATGCTGAAG
7801 ATCAGTTGGG CGCACGAGTG GGTACATCG AACTGGATCT CAACAGCGGT AAGATCCTTG
7861 AGAGTTTTTCG CCCCAGAGAA CGTTTTCCAA TGATGAGCAC TTTTAAAGTT CTGCTATGTC
7921 ATACACTATT ATCCCGTATT GACGCCGGG AAGAGCAACT CGGTCGCCGG GCGCGGTATT
20 7981 CTCAGAATGA CTTGGTTGAG TACTCACCAG TCACAGAAAA GCATCTTACG GATGGCATGA
8041 CAGTAAGAGA ATTATGCAGT GCTGCCATAA CCATGAGTGA TAACACTGCG GCCAACTTAC
8101 TTCTGACAAC GATCGGAGGA CCGAAGGAGC TAACCGCTTT TTTGCACAAC ATGGGGGATC
8161 ATGTAACCTG CTTGATCGT TGGGAACCGG AGCTGAATGA AGCCATACCA AACGACGAGC
8221 GTGACACCAC GATGCCTGTA GCAATGCCAA CAACGTTGCG CAACTATTA ACTGGCGAAC
25 8281 TACTTACTCT AGCTTCCCGG CAACAATTAA TAGACTGGAT GGAGGCGGAT AAAGTTGCAG
8341 GACCACTTCT GCGCTCGGCC CTTCCGGCTG GCTGGTTTAT TGCTGATAAA TCTGGAGCCG
8401 GTGAGCGTGG GTCTCGCGGT ATCATTGCAG CACTGGGGCC AGATGGTAAG CCCTCCCGTA
8461 TCGTAGTTAT CTACACGACG GGGAGTCAGG CAACTATGGA TGAACGAAAT AGACAGATCG
8521 CTGAGATAGG TGCCTCACTG ATTAAGCATT GGTAAGTGT AGACCAAGTT TACTCATATA
30 8581 TACTTTAGAT TGATTTAAAA CTTCAATTTT AATTTAAAAG GATCTAGGTG AAGATCCTTT
8641 TTGATAATCT CATGACCAAA ATCCCTTAAC GTGAGTTTTT GTTCCACTGT ACGTAAGACC
8701 CCAAGCTTG TCGACTGAAT GGCGAATGGC GCTTTGCCTG GTTCCGGCA CCAGAAGCGG
8761 TGCCGGAAG CTGGCTGGAG TGCGATCTTC CTGAGGCCGA TACTGTCGTC GTCCCTCAA
8821 ACTGGCAGAT GCACGGTTAC GATGCGCCCA TCTACACCAA CGTAACCTAT CCCATTACGG
35 8881 TCAATCCGCC GTTTGTTCCC ACGGAGAATC CGACGGGTTG TTAATCGCTC ACATTTAATG
8941 TTGATGAAAG CTGGCTACAG GAAGGCCAGA CGCGAATTAT TTTTGATGGC GTTCCTATTG
9001 GTTAAAAAAT GAGCTGATTT AACAAAAAT TAACGCGAAT TTTAACAAAA TATTAACGTT
9061 TACAATTTAA ATATTTGCTT ATACAATCTT CCTGTTTTTG GGGCTTTTCT GATTATCAAC
9121 CGGGGTACAT ATGATTGACA TGCTAGTTTT ACGATTACCG TTCATCGATT CTCTGTTTTG

5

9181 CTCCAGACTC TCAGGCAATG ACCTGATAGC CTTTGTAGAT CTCTCAAAAA TAGCTACCCT
9241 CTCCGGCATG AATTTATCAG CTAGAACGGT TGAATATCAT ATTGATGGTG ATTTGACTGT
9301 CTCCGGCCTT TCTCACCCCTT TTGAATCTTT ACCTACACAT TACTCAGGCA TTGCATTTAA
9361 AATATATGAG GGTTCATAAA ATTTTATCC TTGCGTTGAA ATAAAGGCTT CTCCCGCAA
9421 AGTATTACAG GGCATAATG TTTTGGTAC AACCGATTTA GCTTTATGCT CTGAGGCTTT
9481 ATTGCTTAAT TTTGCTAATT CTTTGCCTTG CCTGTATGAT TTATTGGATG TT

Table 200: Enzymes that either cut 15 or more human GLGs or have 5+-base recognition in FR3

Typical entry:

REname Recognition #sites
 GLGid#:base# GLGid#:base# GLGid#:base#.....

5

BstEII Ggtnacc 2
 1: 3 48: 3
 There are 2 hits at base# 3

10

MaeIII gtnac 36
 1: 4 2: 4 3: 4 4: 4 5: 4 6: 4
 7: 4 8: 4 9: 4 10: 4 11: 4 37: 4
 37: 58 38: 4 38: 58 39: 4 39: 58 40: 4
 40: 58 41: 4 41: 58 42: 4 42: 58 43: 4
 43: 58 44: 4 44: 58 45: 4 45: 58 46: 4
 46: 58 47: 4 47: 58 48: 4 49: 4 50: 58
 There are 24 hits at base# 4

15

Tsp45I gtsac 33
 1: 4 2: 4 3: 4 4: 4 5: 4 6: 4
 7: 4 8: 4 9: 4 10: 4 11: 4 37: 4
 37: 58 38: 4 38: 58 39: 58 40: 4 40: 58
 41: 58 42: 58 43: 4 43: 58 44: 4 44: 58
 45: 4 45: 58 46: 4 46: 58 47: 4 47: 58
 48: 4 49: 4 50: 58
 There are 21 hits at base# 4

20

25

HphI tcacc 45
 1: 5 2: 5 3: 5 4: 5 5: 5 6: 5
 7: 5 8: 5 11: 5 12: 5 12: 11 13: 5
 14: 5 15: 5 16: 5 17: 5 18: 5 19: 5
 20: 5 21: 5 22: 5 23: 5 24: 5 25: 5
 26: 5 27: 5 28: 5 29: 5 30: 5 31: 5
 32: 5 33: 5 34: 5 35: 5 36: 5 37: 5
 38: 5 40: 5 43: 5 44: 5 45: 5 46: 5
 47: 5 48: 5 49: 5
 There are 44 hits at base# 5

30

35

NlaIII CATG

26

1: 9 1: 42 2: 42 3: 9 3: 42 4: 9
 4: 42 5: 9 5: 42 6: 42 6: 78 7: 9
 7: 42 8: 21 8: 42 9: 42 10: 42 11: 42
 5 12: 57 13: 48 13: 57 14: 57 31: 72 38: 9
 48: 78 49: 78

There are 11 hits at base# 42

There are 1 hits at base# 48 Could cause raggedness.

10 BsaJI Ccnngg

37

1: 14 2: 14 5: 14 6: 14 7: 14 8: 14
 8: 65 9: 14 10: 14 11: 14 12: 14 13: 14
 14: 14 15: 65 17: 14 17: 65 18: 65 19: 65
 20: 65 21: 65 22: 65 26: 65 29: 65 30: 65
 15 33: 65 34: 65 35: 65 37: 65 38: 65 39: 65
 40: 65 42: 65 43: 65 48: 65 49: 65 50: 65
 51: 14

There are 23 hits at base# 65

There are 14 hits at base# 14

20

AluI AGct

42

1: 47 2: 47 3: 47 4: 47 5: 47 6: 47
 7: 47 8: 47 9: 47 10: 47 11: 47 16: 63
 23: 63 24: 63 25: 63 31: 63 32: 63 36: 63
 25 37: 47 37: 52 38: 47 38: 52 39: 47 39: 52
 40: 47 40: 52 41: 47 41: 52 42: 47 42: 52
 43: 47 43: 52 44: 47 44: 52 45: 47 45: 52
 46: 47 46: 52 47: 47 47: 52 49: 15 50: 47

There are 23 hits at base# 47

30 There are 11 hits at base# 52 Only 5 bases from 47

BlnI GCtnagc

21

1: 48 2: 48 3: 48 5: 48 6: 48 7: 48
 8: 48 9: 48 10: 48 11: 48 37: 48 38: 48
 35 39: 48 40: 48 41: 48 42: 48 43: 48 44: 48
 45: 48 46: 48 47: 48

There are 21 hits at base# 48

MwoI GCNNNNNnngc

19

1: 48 2: 28 19: 36 22: 36 23: 36 24: 36

25: 36 26: 36 35: 36 37: 67 39: 67 40: 67

41: 67 42: 67 43: 67 44: 67 45: 67 46: 67

5 47: 67

There are 10 hits at base# 67

There are 7 hits at base# 36

DdeI Ctnag

71

10 1: 49 1: 58 2: 49 2: 58 3: 49 3: 58

3: 65 4: 49 4: 58 5: 49 5: 58 5: 65

6: 49 6: 58 6: 65 7: 49 7: 58 7: 658: 49 8: 58 9: 49 9: 58 9: 65 10: 4910: 58 10: 65 11: 49 11: 58 11: 65 15: 5815 16: 58 16: 65 17: 58 18: 58 20: 58 21: 5822: 58 23: 58 23: 65 24: 58 24: 65 25: 5825: 65 26: 58 27: 58 27: 65 28: 58 30: 5831: 58 31: 65 32: 58 32: 65 35: 58 36: 5836: 65 37: 49 38: 49 39: 26 39: 49 40: 49

20 41: 49 42: 26 42: 49 43: 49 44: 49 45: 49

46: 49 47: 49 48: 12 49: 12 51: 65

There are 29 hits at base# 58

There are 22 hits at base# 49 Only nine base from 58There are 16 hits at base# 65 Only seven bases from 58

25

BglII Agatct

11

1: 61 2: 61 3: 61 4: 61 5: 61 6: 61

7: 61 9: 61 10: 61 11: 61 51: 47

There are 10 hits at base# 61

30

BstYI Rgatcy

12

1: 61 2: 61 3: 61 4: 61 5: 61 6: 61

7: 61 8: 61 9: 61 10: 61 11: 61 51: 47

There are 11 hits at base# 61

35

Hpy188I TCNga 17
 1: 64 2: 64 3: 64 4: 64 5: 64 6: 64
 7: 64 8: 64 9: 64 10: 64 11: 64 16: 57
 20: 57 27: 57 35: 57 48: 67 49: 67

5 There are 11 hits at base# 64
 There are 4 hits at base# 57
 There are 2 hits at base# 67 Could be ragged.

MslI CAYNNnnRTG 44
 10 1: 72 2: 72 3: 72 4: 72 5: 72 6: 72
 7: 72 8: 72 9: 72 10: 72 11: 72 15: 72
 17: 72 18: 72 19: 72 21: 72 23: 72 24: 72
 25: 72 26: 72 28: 72 29: 72 30: 72 31: 72
 32: 72 33: 72 34: 72 35: 72 36: 72 37: 72
 15 38: 72 39: 72 40: 72 41: 72 42: 72 43: 72
 44: 72 45: 72 46: 72 47: 72 48: 72 49: 72
 50: 72 51: 72
 There are 44 hits at base# 72

20 BsiEI CGRYcg 23
 1: 74 3: 74 4: 74 5: 74 7: 74 8: 74
 9: 74 10: 74 11: 74 17: 74 22: 74 30: 74
 33: 74 34: 74 37: 74 38: 74 39: 74 40: 74
 41: 74 42: 74 45: 74 46: 74 47: 74
 25 There are 23 hits at base# 74

EaeI Yggccr 23
 1: 74 3: 74 4: 74 5: 74 7: 74 8: 74
 9: 74 10: 74 11: 74 17: 74 22: 74 30: 74
 30 33: 74 34: 74 37: 74 38: 74 39: 74 40: 74
 41: 74 42: 74 45: 74 46: 74 47: 74
 There are 23 hits at base# 74

EagI Cggccg 23
 35 1: 74 3: 74 4: 74 5: 74 7: 74 8: 74
 9: 74 10: 74 11: 74 17: 74 22: 74 30: 74

33: 74 34: 74 37: 74 38: 74 39: 74 40: 74
 41: 74 42: 74 45: 74 46: 74 47: 74

There are 23 hits at base# 74

5 HaeIII GGcc

27

1: 75 3: 75 4: 75 5: 75 7: 75 8: 75
 9: 75 10: 75 11: 75 16: 75 17: 75 20: 75
 22: 75 30: 75 33: 75 34: 75 37: 75 38: 75
 39: 75 40: 75 41: 75 42: 75 45: 75 46: 75

10 47: 75 48: 63 49: 63

There are 25 hits at base# 75

Bst4CI ACNgt 65°C

63 Sites There is a third isoschismer

1: 86 2: 86 3: 86 4: 86 5: 86 6: 86
 15 7: 34 7: 86 8: 86 9: 86 10: 86 11: 86
 12: 86 13: 86 14: 86 15: 36 15: 86 16: 53
 16: 86 17: 36 17: 86 18: 86 19: 86 20: 53
 20: 86 21: 36 21: 86 22: 0 22: 86 23: 86
 24: 86 25: 86 26: 86 27: 53 27: 86 28: 36
 20 28: 86 29: 86 30: 86 31: 86 32: 86 33: 36
 33: 86 34: 86 35: 53 35: 86 36: 86 37: 86
 38: 86 39: 86 40: 86 41: 86 42: 86 43: 86
 44: 86 45: 86 46: 86 47: 86 48: 86 49: 86
 50: 86 51: 0 51: 86

25 There are 51 hits at base# 86 All the other sites are well away

HpyCH4III ACNgt

63

1: 86 2: 86 3: 86 4: 86 5: 86 6: 86
 7: 34 7: 86 8: 86 9: 86 10: 86 11: 86
 30 12: 86 13: 86 14: 86 15: 36 15: 86 16: 53
 16: 86 17: 36 17: 86 18: 86 19: 86 20: 53
 20: 86 21: 36 21: 86 22: 0 22: 86 23: 86
 24: 86 25: 86 26: 86 27: 53 27: 86 28: 36
 28: 86 29: 86 30: 86 31: 86 32: 86 33: 36
 35 33: 86 34: 86 35: 53 35: 86 36: 86 37: 86
 38: 86 39: 86 40: 86 41: 86 42: 86 43: 86

44: 86 45: 86 46: 86 47: 86 48: 86 49: 86

50: 86 51: 0 51: 86

There are 51 hits at base# 86

5 HinfI Gantc

43

2: 2 3: 2 4: 2 5: 2 6: 2 7: 2

8: 2 9: 2 9: 22 10: 2 11: 2 15: 2

16: 2 17: 2 18: 2 19: 2 19: 22 20: 2

21: 2 23: 2 24: 2 25: 2 26: 2 27: 2

10 28: 2 29: 2 30: 2 31: 2 32: 2 33: 2

33: 22 34: 22 35: 2 36: 2 37: 2 38: 2

40: 2 43: 2 44: 2 45: 2 46: 2 47: 2

50: 60

There are 38 hits at base# 2

15

MlyI GAGTCNNNNNn

18

2: 2 3: 2 4: 2 5: 2 6: 2 7: 2

8: 2 9: 2 10: 2 11: 2 37: 2 38: 2

40: 2 43: 2 44: 2 45: 2 46: 2 47: 2

20 There are 18 hits at base# 2

PleI gagtc

18

2: 2 3: 2 4: 2 5: 2 6: 2 7: 2

8: 2 9: 2 10: 2 11: 2 37: 2 38: 2

25 40: 2 43: 2 44: 2 45: 2 46: 2 47: 2

There are 18 hits at base# 2

AciI Ccgc

24

2: 26 9: 14 10: 14 11: 14 27: 74 37: 62

37: 65 38: 62 39: 65 40: 62 40: 65 41: 65

30 42: 65 43: 62 43: 65 44: 62 44: 65 45: 62

46: 62 47: 62 47: 65 48: 35 48: 74 49: 74

There are 8 hits at base# 62

There are 8 hits at base# 65

There are 3 hits at base# 14

35 There are 3 hits at base# 74

There are 1 hits at base# 26

There are 1 hits at base# 35

-- Gcgg 11
 8: 91 9: 16 10: 16 11: 16 37: 67 39: 67
 40: 67 42: 67 43: 67 45: 67 46: 67

There are 7 hits at base# 67

5 There are 3 hits at base# 16
 There are 1 hits at base# 91

BsiHKAI GWGCWc 20
 2: 30 4: 30 6: 30 7: 30 9: 30 10: 30
 10 12: 89 13: 89 14: 89 37: 51 38: 51 39: 51
 40: 51 41: 51 42: 51 43: 51 44: 51 45: 51
 46: 51 47: 51
 There are 11 hits at base# 51

15 Bsp1286I GDGCHc 20
 2: 30 4: 30 6: 30 7: 30 9: 30 10: 30
 12: 89 13: 89 14: 89 37: 51 38: 51 39: 51
 40: 51 41: 51 42: 51 43: 51 44: 51 45: 51
 46: 51 47: 51
 20 There are 11 hits at base# 51

HgiAI GWGCWc 20
 2: 30 4: 30 6: 30 7: 30 9: 30 10: 30
 12: 89 13: 89 14: 89 37: 51 38: 51 39: 51
 25 40: 51 41: 51 42: 51 43: 51 44: 51 45: 51
 46: 51 47: 51
 There are 11 hits at base# 51

BsoFI GCngc 26
 30 2: 53 3: 53 5: 53 6: 53 7: 53 8: 53
 8: 91 9: 53 10: 53 11: 53 31: 53 36: 36
 37: 64 39: 64 40: 64 41: 64 42: 64 43: 64
 44: 64 45: 64 46: 64 47: 64 48: 53 49: 53
 50: 45 51: 53
 35 There are 13 hits at base# 53
 There are 10 hits at base# 64

TseI GcwgC 17
 2: 53 3: 53 5: 53 6: 53 7: 53 8: 53

9: 53 10: 53 11: 53 31: 53 36: 36 45: 64
 46: 64 48: 53 49: 53 50: 45 51: 53

There are 13 hits at base# 53

5 MnlI gagg

34

3: 67 3: 95 4: 51 5: 16 5: 67 6: 67
 7: 67 8: 67 9: 67 10: 67 11: 67 15: 67
 16: 67 17: 67 19: 67 20: 67 21: 67 22: 67
 23: 67 24: 67 25: 67 26: 67 27: 67 28: 67
 29: 67 30: 67 31: 67 32: 67 33: 67 34: 67
 35: 67 36: 67 50: 67 51: 67

There are 31 hits at base# 67

HpyCH4V TGca

34

5: 90 6: 90 11: 90 12: 90 13: 90 14: 90
 15: 44 16: 44 16: 90 17: 44 18: 90 19: 44
 20: 44 21: 44 22: 44 23: 44 24: 44 25: 44
 26: 44 27: 44 27: 90 28: 44 29: 44 33: 44
 34: 44 35: 44 35: 90 36: 38 48: 44 49: 44
 50: 44 50: 90 51: 44 51: 52

There are 21 hits at base# 44

There are 1 hits at base# 52

AccI GTmkac

13 5-base recognition

7: 37 11: 24 37: 16 38: 16 39: 16 40: 16
 41: 16 42: 16 43: 16 44: 16 45: 16 46: 16
 47: 16

There are 11 hits at base# 16

30 SacII CCGCgg

8 6-base recognition

9: 14 10: 14 11: 14 37: 65 39: 65 40: 65
 42: 65 43: 65

There are 5 hits at base# 65

There are 3 hits at base# 14

35

TfiI Gawtc

24

9: 22 15: 2 16: 2 17: 2 18: 2 19: 2
 19: 22 20: 2 21: 2 23: 2 24: 2 25: 2

26: 2 27: 2 28: 2 29: 2 30: 2 31: 2

32: 2 33: 2 33: 22 34: 22 35: 2 36: 2

There are 20 hits at base# 2

5 BsmAI Nnnnnngagac 19
 15: 11 16: 11 20: 11 21: 11 22: 11 23: 11
 24: 11 25: 11 26: 11 27: 11 28: 11 28: 56
 30: 11 31: 11 32: 11 35: 11 36: 11 44: 87
 48: 87

10 There are 16 hits at base# 11

BpmI ctccag 19
 15: 12 16: 12 17: 12 18: 12 20: 12 21: 12
 22: 12 23: 12 24: 12 25: 12 26: 12 27: 12
 15 28: 12 30: 12 31: 12 32: 12 34: 12 35: 12
 36: 12

There are 19 hits at base# 12

XmnI GAANNnnttc 12
 20 37: 30 38: 30 39: 30 40: 30 41: 30 42: 30
 43: 30 44: 30 45: 30 46: 30 47: 30 50: 30
 There are 12 hits at base# 30

BsrI NCcagt 12
 25 37: 32 38: 32 39: 32 40: 32 41: 32 42: 32
 43: 32 44: 32 45: 32 46: 32 47: 32 50: 32
 There are 12 hits at base# 32

BanII GRGcYc 11
 30 37: 51 38: 51 39: 51 40: 51 41: 51 42: 51
 43: 51 44: 51 45: 51 46: 51 47: 51
 There are 11 hits at base# 51

Ecl136I GAGctc 11
 35 37: 51 38: 51 39: 51 40: 51 41: 51 42: 51
 43: 51 44: 51 45: 51 46: 51 47: 51
 There are 11 hits at base# 51

SacI GAGCTc 11

37: 51 38: 51 39: 51 40: 51 41: 51 42: 51

43: 51 44: 51 45: 51 46: 51 47: 51

There are 11 hits at base# 51

Table 217: Human HC GLG FR1 Sequences

VH Exon - Nucleotide sequence alignment

VH1

5	1-02	CAG GTG CAG CTG GTG CAG TCT GGG GCT GAG GTG AAG AAG CCT GGG GCC TCA GTG AAG GTC TCC TGC AAG GCT TCT GGA TAC ACC TTC ACC
	1-03	cag gtC cag ctT gtg cag tct ggg gct gag gtg aag aag cct ggg gcc tca gtg aag gtT tcc tgc aag gct tct gga tac acc ttc acT
	1-08	cag gtg cag ctg gtg cag tct ggg gct gag gtg aag aag cct ggg gcc tca gtg aag gtc tcc tgc aag gct tct gga tac acc ttc acc
10	1-18	cag gtT cag ctg gtg cag tct ggA gct gag gtg aag aag cct ggg gcc tca gtg aag gtc tcc tgc aag gct tct ggT tac acc ttT acc
	1-24	cag gtC cag ctg gtA cag tct ggg gct gag gtg aag aag cct ggg gcc tca gtg aag gtc tcc tgc aag gTt tC gga tac acc Ctc acT
	1-45	cag Atg cag ctg gtg cag tct ggg gct gag gtg aag aag Act ggg Tcc tca gtg aag gtT tcc tgc aag gct tC gga tac acc ttc acc
15	1-46	cag gtg cag ctg gtg cag tct ggg gct gag gtg aag aag cct ggg gcc tca gtg aag gtT tcc tgc aag gC A tct gga tac acc ttc acc
	1-58	caA Atg cag ctg gtg cag tct ggg Cct gag gtg aag aag cct ggg Acc tca gtg aag gtc tcc tgc aag gct tct gga tTc acc ttT acT
	1-69	cag gtg cag ctg gtg cag tct ggg gct gag gtg aag aag cct ggg Tcc tCg gtg aag gtc tcc tgc aag gct tct gga GGc acc ttc aGc
20	1-e	cag gtg cag ctg gtg cag tct ggg gct gag gtg aag aag cct ggg Tcc tCg gtg aag gtc tcc tgc aag gct tct gga GGc acc ttc aGc
	1-f	Gag gtC cag ctg gtA cag tct ggg gct gag gtg aag aag cct ggg gCT Aca gtg aaA Atc tcc tgc aag gTt tct gga tac acc ttc acc
	1-f	Gag gtC cag ctg gtA cag tct ggg gct gag gtg aag aag cct ggg gCT Aca gtg aaA Atc tcc tgc aag gTt tct gga tac acc ttc acc
25	1-f	Gag gtC cag ctg gtA cag tct ggg gct gag gtg aag aag cct ggg gCT Aca gtg aaA Atc tcc tgc aag gTt tct gga tac acc ttc acc
	1-f	Gag gtC cag ctg gtA cag tct ggg gct gag gtg aag aag cct ggg gCT Aca gtg aaA Atc tcc tgc aag gTt tct gga tac acc ttc acc
	1-f	Gag gtC cag ctg gtA cag tct ggg gct gag gtg aag aag cct ggg gCT Aca gtg aaA Atc tcc tgc aag gTt tct gga tac acc ttc acc
30	2-05	CAG ATC ACC TTG AAG GAG TCT GGT CCT ACG CTG GTG AAA CCC ACA CAG ACC CTC ACG CTG ACC TGC ACC TTC TCT GGG TTC TCA CTC AGC
	2-26	cag Gtc acc ttg aag gag tct ggt cct GTg ctg gtg aaa ccc aca Gag acc ctc acg ctg acc tgc acc Gtc tct ggg ttc tca ctc agc
	2-70	cag Gtc acc ttg aag gag tct ggt cct Gcg ctg gtg aaa ccc aca cag acc ctc acA ctg acc tgc acc ttc tct ggg ttc tca ctc agc
35	3-07	GAG GTG CAG CTG GTG GAG TCT GGG GGA GGC TTG GTC CAG CCT GGG GGG TCC CTG AGA CTC TCC TGT GCA GCC TCT GGA TTC ACC TTT AGT
	3-09	gaA gtg cag ctg gtg gag tct ggg gga ggc ttg gtA cag cct ggC Agg tcc ctg aga ctc tcc tgt gca gcc tct gga ttc acc ttt GAt
	3-11	Cag gtg cag ctg gtg gag tct ggg gga ggc ttg gtc Aag cct ggA ggg tcc ctg aga ctc tcc tgt gca gcc tct gga ttc acc ttC agt
40	3-13	gag gtg cag ctg gtg gag tct ggg gga ggc ttg gtA cag cct ggg ggg tcc ctg aga ctc tcc tgt gca gcc tct gga ttc acc ttC agt
	3-15	gag gtg cag ctg gtg gag tct ggg gga ggc ttg gtA Aag cct ggg ggg tcc ctT aga ctc tcc tgt gca gcc tct gga ttc acT ttC agt
	3-20	gag gtg cag ctg gtg gag tct ggg gga ggT Gtg gtA cGg cct ggg ggg tcc ctg aga

ctc tcc tgt gca gcc tct gga ttc acc ttt GAt
 3-21 gag gtg cag ctg gtg gag tct ggg gga ggc Ctg gtc Aag cct ggg ggg. tcc ctg aga
 ctc tcc tgt gca gcc tct gga ttc acc ttC agt
 3-23 gag gtg cag ctg Ttg gag tct ggg gga ggc ttg gtA cag cct ggg ggg tcc ctg aga
 5 ctc tcc tgt gca gcc tct gga ttc acc ttt agC
 3-30 Cag gtg cag ctg gtg gag tct ggg gga ggc Gtg gtc cag cct ggg Agg tcc ctg aga
 ctc tcc tgt gca gcc tct gga ttc acc ttC agt
 3-30.3 Cag gtg cag ctg gtg gag tct ggg gga ggc Gtg gtc cag cct ggg Agg tcc ctg aga
 ctc tcc tgt gca gcc tct gga ttc acc ttC agt
 10 3-30.5 Cag gtg cag ctg gtg gag tct ggg gga ggc Gtg gtc cag cct ggg Agg tcc ctg aga
 ctc tcc tgt gca gcc tct gga ttc acc ttC agt
 3-33 Cag gtg cag ctg gtg gag tct ggg gga ggc Gtg gtc cag cct ggg Agg tcc ctg aga
 ctc tcc tgt gca gcG tct gga ttc acc ttC agt
 3-43 gaA gtg cag ctg gtg gag tct ggg gga gTc Gtg gtA cag cct ggg ggg tcc ctg aga
 15 ctc tcc tgt gca gcc tct gga ttc acc ttt GAt
 3-48 gag gtg cag ctg gtg gag tct ggg gga ggc ttg gtA cag cct ggg ggg tcc ctg aga
 ctc tcc tgt gca gcc tct gga ttc acc ttC agt
 3-49 gag gtg cag ctg gtg gag tct ggg gga ggc ttg gtA cag ccA ggg Cgg tcc ctg aga
 ctc tcc tgt Aca gcT tct gga ttc acc ttt Ggt
 20 3-53 gag gtg cag ctg gtg gag Act ggA gga ggc ttg Atc cag cct ggg ggg tcc ctg aga
 ctc tcc tgt gca gcc tct ggG ttc acc GtC agt
 3-64 gag gtg cag ctg gtg gag tct ggg gga ggc ttg gtc cag cct ggg ggg tcc ctg aga
 ctc tcc tgt gca gcc tct gga ttc acc ttC agt
 3-66 gag gtg cag ctg gtg gag tct ggg gga ggc ttg gtc cag cct ggg ggg tcc ctg aga
 25 ctc tcc tgt gca gcc tct gga ttc acc GtC agt
 3-72 gag gtg cag ctg gtg gag tct ggg gga ggc ttg gtc cag cct ggA ggg tcc ctg aga
 ctc tcc tgt gca gcc tct gga ttc acc ttC agt
 3-73 gag gtg cag ctg gtg gag tct ggg gga ggc ttg gtc cag cct ggg ggg tcc ctg aAa
 ctc tcc tgt gca gcc tct ggG ttc acc ttC agt
 30 3-74 gag gtg cag ctg gtg gag tC C ggg gga ggc ttA gtT cag cct ggg ggg tcc ctg aga
 ctc tcc tgt gca gcc tct gga ttc acc ttC agt
 3-d gag gtg cag ctg gtg gag tct Cgg gga gTc ttg gtA cag cct ggg ggg tcc ctg aga
 ctc tcc tgt gca gcc tct gga ttc acc GtC agt
 VH4
 35 4-04 CAG GTG CAG CTG CAG GAG TCG GGC CCA GGA CTG GTG AAG CCT TCG GGG ACC CTG TCC
 CTC ACC TGC GCT GTC TCT GGT GGC TCC ATC AGC
 4-28 cag gtg cag ctg cag gag tCg ggc cca gga ctg gtg aag cct tCg gAC acc ctg tcc
 ctc acc tgc gct gtc tct ggt TAc tcc atc agc
 4-30.1 cag gtg cag ctg cag gag tCg ggc cca gga ctg gtg aag cct tC A CAg acc ctg tcc
 40 ctc acc tgc Act gtc tct ggt ggc tcc atc agc
 4-30.2 cag Ctg cag ctg cag gag tC C ggc Tcà gga ctg gtg aag cct tC A CAg acc ctg tcc
 ctc acc tgc gct gtc tct ggt ggc tcc atc agc
 4-30.4 cag gtg cag ctg cag gag tCg ggc cca gga ctg gtg aag cct tC A CAg acc ctg tcc
 ctc acc tgc Act gtc tct ggt ggc tcc atc agc

4-31 cag gtg cag ctg cag gag tcg ggc cca gga ctg gtg aag cct tcA CAg acc ctg tcc
 ctc acc tgc Act gtc tct ggt ggc tcc atc agc
 4-34 cag gtg cag ctA cag Cag tGg ggc Gca gga ctg Ttg aag cct tcg gAg acc ctg tcc
 ctc acc tgc gct gtc tAt ggt ggG tcc Ttc agT
 5 4-39 cag Ctg cag ctg cag gag tcg ggc cca gga ctg gtg aag cct tcg gAg acc ctg tcc
 ctc acc tgc Act gtc tct ggt ggc tcc atc agc
 4-59 cag gtg cag ctg cag gag tcg ggc cca gga ctg gtg aag cct tcg gAg acc ctg tcc
 ctc acc tgc Act gtc tct ggt ggc tcc atc agT
 10 4-61 cag gtg cag ctg cag gag tcg ggc cca gga ctg gtg aag cct tcg gAg acc ctg tcc
 ctc acc tgc Act gtc tct ggt ggc tcc Gtc agc
 4-b cag gtg cag ctg cag gag tcg ggc cca gga ctg gtg aag cct tcg gAg acc ctg tcc
 ctc acc tgc gct gtc tct ggt TAc tcc atc agc
 VH5
 15 5-51 GAG GTG CAG CTG GTG CAG TCT GGA GCA GAG GTG AAA AAG CCC GGG GAG TCT CTG AAG
 ATC TCC TGT AAG GGT TCT GGA TAC AGC TTT ACC
 5-a gaA gtg cag ctg gtg cag tct gga gca gag gtg aaa aag ccc ggg gag tct ctg aGg
 atc tcc tgt aag ggt tct gga tac agc ttt acc
 VH6
 20 6-1 CAG GTA CAG CTG CAG CAG TCA GGT CCA GGA CTG GTG AAG CCC TCG CAG ACC CTC TCA
 CTC ACC TGT GCC ATC TCC GGG GAC AGT GTC TCT
 VH7
 7-4.1 CAG GTG CAG CTG GTG CAA TCT GGG TCT GAG TTG AAG AAG CCT GGG GCC TCA GTG AAG
 GTT TCC TGC AAG GCT TCT GGA TAC ACC TTC ACT

Table 220: RERS sites in Human HC GLG FR1s where there are at least 20 GLGs cut

BsgI GTGCAG 71 (cuts 16/14 bases to right)

	1: 4	1: 13	2: 13	3: 4	3: 13	4: 13
	6: 13	7: 4	7: 13	8: 13	9: 4	9: 13
5	10: 4	10: 13	15: 4	15: 65	16: 4	16: 65
	17: 4	17: 65	18: 4	18: 65	19: 4	19: 65
	20: 4	20: 65	21: 4	21: 65	22: 4	22: 65
	23: 4	23: 65	24: 4	24: 65	25: 4	25: 65
	26: 4	26: 65	27: 4	27: 65	28: 4	28: 65
10	29: 4	30: 4	30: 65	31: 4	31: 65	32: 4
	32: 65	33: 4	33: 65	34: 4	34: 65	35: 4
	35: 65	36: 4	36: 65	37: 4	38: 4	39: 4
	41: 4	42: 4	43: 4	45: 4	46: 4	47: 4
	48: 4	48: 13	49: 4	49: 13	51: 4	

15 There are 39 hits at base# 4

There are 21 hits at base# 65

	-"- ctgcac	9				
	12: 63	13: 63	14: 63	39: 63	41: 63	42: 63
20	44: 63	45: 63	46: 63			

	BbvI GCAGC	65				
	1: 6	3: 6	6: 6	7: 6	8: 6	9: 6
	10: 6	15: 6	15: 67	16: 6	16: 67	17: 6
	17: 67	18: 6	18: 67	19: 6	19: 67	20: 6
25	20: 67	21: 6	21: 67	22: 6	22: 67	23: 6
	23: 67	24: 6	24: 67	25: 6	25: 67	26: 6
	26: 67	27: 6	27: 67	28: 6	28: 67	29: 6
	30: 6	30: 67	31: 6	31: 67	32: 6	32: 67
	33: 6	33: 67	34: 6	34: 67	35: 6	35: 67
30	36: 6	36: 67	37: 6	38: 6	39: 6	40: 6
	41: 6	42: 6	43: 6	44: 6	45: 6	46: 6
	47: 6	48: 6	49: 6	50: 12	51: 6	

There are 43 hits at base# 6 Boded sites very near sites
listed below

35 There are 21 hits at base# 67

	-"- gctgc	13				
	37: 9	38: 9	39: 9	40: 3	40: 9	41: 9
	42: 9	44: 3	44: 9	45: 9	46: 9	47: 9

50: 9

There are 11 hits at base# 9

BsoFI GCngc

78

5 1: 6 3: 6 6: 6 7: 6 8: 6 9: 6
 10: 6 15: 6 15: 67 16: 6 16: 67 17: 6
 17: 67 18: 6 18: 67 19: 6 19: 67 20: 6
 20: 67 21: 6 21: 67 22: 6 22: 67 23: 6
 23: 67 24: 6 24: 67 25: 6 25: 67 26: 6
 10 26: 67 27: 6 27: 67 28: 6 28: 67 29: 6
 30: 6 30: 67 31: 6 31: 67 32: 6 32: 67
 33: 6 33: 67 34: 6 34: 67 35: 6 35: 67
 36: 6 36: 67 37: 6 37: 9 38: 6 38: 9
 39: 6 39: 9 40: 3 40: 6 40: 9 41: 6
 15 41: 9 42: 6 42: 9 43: 6 44: 3 44: 6
44: 9 45: 6 45: 9 46: 6 46: 9 47: 6
47: 9 48: 6 49: 6 50: 9 50: 12 51: 6

There are 43 hits at base# 6 These often occur together.

There are 11 hits at base# 9

20 There are 2 hits at base# 3

There are 21 hits at base# 67

TseI GcwgC

78

1: 6 3: 6 6: 6 7: 6 8: 6 9: 6
 25 10: 6 15: 6 15: 67 16: 6 16: 67 17: 6
 17: 67 18: 6 18: 67 19: 6 19: 67 20: 6
 20: 67 21: 6 21: 67 22: 6 22: 67 23: 6
 23: 67 24: 6 24: 67 25: 6 25: 67 26: 6
 26: 67 27: 6 27: 67 28: 6 28: 67 29: 6
 30 30: 6 30: 67 31: 6 31: 67 32: 6 32: 67
 33: 6 33: 67 34: 6 34: 67 35: 6 35: 67
 36: 6 36: 67 37: 6 37: 9 38: 6 38: 9
39: 6 39: 9 40: 3 40: 6 40: 9 41: 6
41: 9 42: 6 42: 9 43: 6 44: 3 44: 6
 35 44: 9 45: 6 45: 9 46: 6 46: 9 47: 6
47: 9 48: 6 49: 6 50: 9 50: 12 51: 6

There are 43 hits at base# 6 Often together.

There are 11 hits at base# 9

There are 2 hits at base# 3

There are 1 hits at base# 12

There are 21 hits at base# 67

5 MspAII CMGckg 48

1:	7	3:	7	4:	7	5:	7	6:	7	7:	7
8:	7	9:	7	10:	7	11:	7	15:	7	16:	7
17:	7	18:	7	19:	7	20:	7	21:	7	22:	7
23:	7	24:	7	25:	7	26:	7	27:	7	28:	7
29:	7	30:	7	31:	7	32:	7	33:	7	34:	7
35:	7	36:	7	37:	7	38:	7	39:	7	<u>40:</u>	<u>1</u>
<u>40:</u>	<u>7</u>	41:	7	42:	7	<u>44:</u>	<u>1</u>	<u>44:</u>	<u>7</u>	45:	7
46:	7	47:	7	48:	7	49:	7	50:	7	51:	7

There are 46 hits at base# 7

15 PvuII CAGctg 48

1:	7	3:	7	4:	7	5:	7	6:	7	7:	7
8:	7	9:	7	10:	7	11:	7	15:	7	16:	7
17:	7	18:	7	19:	7	20:	7	21:	7	22:	7
23:	7	24:	7	25:	7	26:	7	27:	7	28:	7
29:	7	30:	7	31:	7	32:	7	33:	7	34:	7
35:	7	36:	7	37:	7	38:	7	39:	7	<u>40:</u>	<u>1</u>
<u>40:</u>	<u>7</u>	41:	7	42:	7	<u>44:</u>	<u>1</u>	<u>44:</u>	<u>7</u>	45:	7
46:	7	47:	7	48:	7	49:	7	50:	7	51:	7

20 There are 46 hits at base# 7

25 There are 2 hits at base# 1

AluI AGct 54

1:	8	2:	8	3:	8	4:	8	4:	24	5:	8
6:	8	7:	8	8:	8	9:	8	10:	8	11:	8
15:	8	16:	8	17:	8	18:	8	19:	8	20:	8
21:	8	22:	8	23:	8	24:	8	25:	8	26:	8
27:	8	28:	8	29:	8	29:	69	30:	8	31:	8
32:	8	33:	8	34:	8	35:	8	36:	8	37:	8
38:	8	39:	8	<u>40:</u>	<u>2</u>	<u>40:</u>	<u>8</u>	41:	8	42:	8
43:	8	<u>44:</u>	<u>2</u>	<u>44:</u>	<u>8</u>	45:	8	46:	8	47:	8
48:	8	48:	82	49:	8	49:	82	50:	8	51:	8

30 There are 48 hits at base# 8

There are 2 hits at base# 2

DdeI Ctnag

48

5 1: 26 1: 48 2: 26 2: 48 3: 26 3: 48
 4: 26 4: 48 5: 26 5: 48 6: 26 6: 48
 7: 26 7: 48 8: 26 8: 48 9: 26 10: 26
 11: 26 12: 85 13: 85 14: 85 15: 52 16: 52
 17: 52 18: 52 19: 52 20: 52 21: 52 22: 52
 23: 52 24: 52 25: 52 26: 52 27: 52 28: 52
 10 29: 52 30: 52 31: 52 32: 52 33: 52 35: 30
 35: 52 36: 52 40: 24 49: 52 51: 26 51: 48

There are 22 hits at base# 52 52 and 48 never together.

There are 9 hits at base# 48

There are 12 hits at base# 26 26 and 24 never together.

15

HphI tcacc

42

1: 86 3: 86 6: 86 7: 86 8: 80 11: 86
 12: 5 13: 5 14: 5 15: 80 16: 80 17: 80
 18: 80 20: 80 21: 80 22: 80 23: 80 24: 80
 20 25: 80 26: 80 27: 80 28: 80 29: 80 30: 80
 31: 80 32: 80 33: 80 34: 80 35: 80 36: 80
 37: 59 38: 59 39: 59 40: 59 41: 59 42: 59
 43: 59 44: 59 45: 59 46: 59 47: 59 50: 59

There are 22 hits at base# 80 80 and 86 never together

25 There are 5 hits at base# 86

There are 12 hits at base# 59

BssKI Nccngg

50

1: 39 2: 39 3: 39 4: 39 5: 39 7: 39
 30 8: 39 9: 39 10: 39 11: 39 15: 39 16: 39
 17: 39 18: 39 19: 39 20: 39 21: 29 21: 39
 22: 39 23: 39 24: 39 25: 39 26: 39 27: 39
 28: 39 29: 39 30: 39 31: 39 32: 39 33: 39
 34: 39 35: 19 35: 39 36: 39 37: 24 38: 24
 35 39: 24 41: 24 42: 24 44: 24 45: 24 46: 24
 47: 24 48: 39 48: 40 49: 39 49: 40 50: 24
 50: 73 51: 39

There are 35 hits at base# 39 39 and 40 together twice.

There are 2 hits at base# 40

BsaJI Ccnnngg 47

5 1: 40 2: 40 3: 40 4: 40 5: 40 7: 40
 8: 40 9: 40 9: 47 10: 40 10: 47 11: 40
 15: 40 18: 40 19: 40 20: 40 21: 40 22: 40
 23: 40 24: 40 25: 40 26: 40 27: 40 28: 40
 29: 40 30: 40 31: 40 32: 40 34: 40 35: 20
 35: 40 36: 40 37: 24 38: 24 39: 24 41: 24
 42: 24 44: 24 45: 24 46: 24 47: 24 48: 40
 10 48: 41 49: 40 49: 41 50: 74 51: 40

There are 32 hits at base# 40 40 and 41 together twice

There are 2 hits at base# 41

There are 9 hits at base# 24

There are 2 hits at base# 47

15

BstNI CCwgg 44

PspGI ccwgg

ScrFI(\$M.HpaII) CCwgg

20 1: 40 2: 40 3: 40 4: 40 5: 40 7: 40
 8: 40 9: 40 10: 40 11: 40 15: 40 16: 40
 17: 40 18: 40 19: 40 20: 40 21: 30 21: 40
 22: 40 23: 40 24: 40 25: 40 26: 40 27: 40
 28: 40 29: 40 30: 40 31: 40 32: 40 33: 40
 34: 40 35: 40 36: 40 37: 25 38: 25 39: 25
 25 41: 25 42: 25 44: 25 45: 25 46: 25 47: 25
 50: 25 51: 40

There are 33 hits at base# 40

ScrFI CCnngg 50

30 1: 40 2: 40 3: 40 4: 40 5: 40 7: 40
 8: 40 9: 40 10: 40 11: 40 15: 40 16: 40
 17: 40 18: 40 19: 40 20: 40 21: 30 21: 40
 22: 40 23: 40 24: 40 25: 40 26: 40 27: 40
 28: 40 29: 40 30: 40 31: 40 32: 40 33: 40
 35 34: 40 35: 20 35: 40 36: 40 37: 25 38: 25
 39: 25 41: 25 42: 25 44: 25 45: 25 46: 25
 47: 25 48: 40 48: 41 49: 40 49: 41 50: 25
 50: 74 51: 40

There are 35 hits at base# 40

There are 2 hits at base# 41

EcoO109I RGgnccy

34

1: 43 2: 43 3: 43 4: 43 5: 43 6: 43
 5 7: 43 8: 43 9: 43 10: 43 15: 46 16: 46
 17: 46 18: 46 19: 46 20: 46 21: 46 22: 46
 23: 46 24: 46 25: 46 26: 46 27: 46 28: 46
 30: 46 31: 46 32: 46 33: 46 34: 46 35: 46
 36: 46 37: 46 43: 79 51: 43

10 There are 22 hits at base# 46 46 and 43 never together

There are 11 hits at base# 43

NlaIV GGNncc

71

1: 43 2: 43 3: 43 4: 43 5: 43 6: 43
 7: 43 8: 43 9: 43 9: 79 10: 43 10: 79
 15: 46 15: 47 16: 47 17: 46 17: 47 18: 46
 18: 47 19: 46 19: 47 20: 46 20: 47 21: 46
 21: 47 22: 46 22: 47 23: 47 24: 47 25: 47
 26: 47 27: 46 27: 47 28: 46 28: 47 29: 47
 30: 46 30: 47 31: 46 31: 47 32: 46 32: 47
 20 33: 46 33: 47 34: 46 34: 47 35: 46 35: 47
 36: 46 36: 47 37: 21 37: 46 37: 47 37: 79
 38: 21 39: 21 39: 79 40: 79 41: 21 41: 79
 42: 21 42: 79 43: 79 44: 21 44: 79 45: 21
 45: 79 46: 21 46: 79 47: 21 51: 43

25 There are 23 hits at base# 47 46 & 47 often together

There are 17 hits at base# 46

There are 11 hits at base# 43

Sau96I Ggncc

70

1: 44 2: 3 2: 44 3: 44 4: 44 5: 3 5: 44 6: 44
 7: 44 8: 22 8: 44 9: 44 10: 44 11: 3 12: 22 13: 22
 30 14: 22 15: 33 15: 47 16: 47 17: 47 18: 47 19: 47 20: 47
 21: 47 22: 47 23: 33 23: 47 24: 33 24: 47 25: 33 25: 47
 26: 33 26: 47 27: 47 28: 47 29: 47 30: 47 31: 33 31: 47
 32: 33 32: 47 33: 33 33: 47 34: 33 34: 47 35: 47 36: 47
 37: 21 37: 22 37: 47 38: 21 38: 22 39: 21 39: 22 41: 21
 35 41: 22 42: 21 42: 22 43: 80 44: 21 44: 22 45: 21 45: 22
 46: 21 46: 22 47: 21 47: 22 50: 22 51: 44

There are 23 hits at base# 47 These do not occur together.

There are 11 hits at base# 44

There are 14 hits at base# 22 These do occur together.

There are 9 hits at base# 21

BsmAI GTCTCNnnnn 22

5 1: 58 3: 58 4: 58 5: 58 8: 58 9: 58
 10: 58 13: 70 36: 18 37: 70 38: 70 39: 70
 40: 70 41: 70 42: 70 44: 70 45: 70 46: 70
 47: 70 48: 48 49: 48 50: 85

There are 11 hits at base# 70

10

--- Nnnnnngagac 27

13: 40 15: 48 16: 48 17: 48 18: 48 20: 48
 21: 48 22: 48 23: 48 24: 48 25: 48 26: 48
 27: 48 28: 48 29: 48 30: 10 30: 48 31: 48
 15 32: 48 33: 48 35: 48 36: 48 43: 40 44: 40
 45: 40 46: 40 47: 40

There are 20 hits at base# 48

AvaII Ggwcc 44

20 Sau96I(\$M.HaeIII) Ggwcc 44

2: 3 5: 3 6: 44 8: 44 9: 44 10: 44
 11: 3 12: 22 13: 22 14: 22 15: 33 15: 47
 16: 47 17: 47 18: 47 19: 47 20: 47 21: 47
 22: 47 23: 33 23: 47 24: 33 24: 47 25: 33
 25 25: 47 26: 33 26: 47 27: 47 28: 47 29: 47
 30: 47 31: 33 31: 47 32: 33 32: 47 33: 33
 33: 47 34: 33 34: 47 35: 47 36: 47 37: 47
 43: 80 50: 22

There are 23 hits at base# 47 44 & 47 never together

30 There are 4 hits at base# 44

PpuMI RGgwccy 27

6: 43 8: 43 9: 43 10: 43 15: 46 16: 46
 17: 46 18: 46 19: 46 20: 46 21: 46 22: 46
 35 23: 46 24: 46 25: 46 26: 46 27: 46 28: 46
 30: 46 31: 46 32: 46 33: 46 34: 46 35: 46
 36: 46 37: 46 43: 79

There are 22 hits at base# 46 43 and 46 never occur together.

There are 4 hits at base# 43

BsmFI GGGAC 3

8: 43 37: 46 50: 77

-"- gtccc 33

5 15: 48 16: 48 17: 48 1: 0 1: 0 20: 48
 21: 48 22: 48 23: 48 24: 48 25: 48 26: 48
 27: 48 28: 48 29: 48 30: 48 31: 48 32: 48
 33: 48 34: 48 35: 48 36: 48 37: 54 38: 54
 39: 54 40: 54 41: 54 42: 54 43: 54 44: 54
 10 45: 54 46: 54 47: 54

There are 20 hits at base# 48

There are 11 hits at base# 54

HinfI Gantc 80

15 8: 77 12: 16 13: 16 14: 16 15: 16 15: 56
 15: 77 16: 16 16: 56 16: 77 17: 16 17: 56
 17: 77 18: 16 18: 56 18: 77 19: 16 19: 56
 19: 77 20: 16 20: 56 20: 77 21: 16 21: 56
 21: 77 22: 16 22: 56 22: 77 23: 16 23: 56
 20 23: 77 24: 16 24: 56 24: 77 25: 16 25: 56
 25: 77 26: 16 26: 56 26: 77 27: 16 27: 26
 27: 56 27: 77 28: 16 28: 56 28: 77 29: 16
 29: 56 29: 77 30: 56 31: 16 31: 56 31: 77
 32: 16 32: 56 32: 77 33: 16 33: 56 33: 77
 25 34: 16 35: 16 35: 56 35: 77 36: 16 36: 26
 36: 56 36: 77 37: 16 38: 16 39: 16 40: 16
 41: 16 42: 16 44: 16 45: 16 46: 16 47: 16
 48: 46 49: 46

There are 34 hits at base# 16

30

TfiI Gawtc 21

8: 77 15: 77 16: 77 17: 77 18: 77 19: 77
 20: 77 21: 77 22: 77 23: 77 24: 77 25: 77
 26: 77 27: 77 28: 77 29: 77 31: 77 32: 77
 35 33: 77 35: 77 36: 77

There are 21 hits at base# 77

MlyI GAGTC 38

12: 16	13: 16	14: 16	15: 16	16: 16	17: 16
18: 16	19: 16	20: 16	21: 16	22: 16	23: 16
24: 16	25: 16	26: 16	27: 16	27: 26	28: 16
29: 16	31: 16	32: 16	33: 16	34: 16	35: 16
36: 16	36: 26	37: 16	38: 16	39: 16	40: 16
41: 16	42: 16	44: 16	45: 16	46: 16	47: 16
48: 46	49: 46				

There are 34 hits at base# 16

10

-"- GACTC 21

15: 56	16: 56	17: 56	18: 56	19: 56	20: 56
21: 56	22: 56	23: 56	24: 56	25: 56	26: 56
27: 56	28: 56	29: 56	30: 56	31: 56	32: 56

15 33: 56 35: 56 36: 56

There are 21 hits at base# 56

PleI gagtc 38

12: 16	13: 16	14: 16	15: 16	16: 16	17: 16
18: 16	19: 16	20: 16	21: 16	22: 16	23: 16
24: 16	25: 16	26: 16	27: 16	27: 26	28: 16
29: 16	31: 16	32: 16	33: 16	34: 16	35: 16
36: 16	36: 26	37: 16	38: 16	39: 16	40: 16
41: 16	42: 16	44: 16	45: 16	46: 16	47: 16
48: 46	49: 46				

There are 34 hits at base# 16

-"- gactc 21

15: 56	16: 56	17: 56	18: 56	19: 56	20: 56
21: 56	22: 56	23: 56	24: 56	25: 56	26: 56
27: 56	28: 56	29: 56	30: 56	31: 56	32: 56
33: 56	35: 56	36: 56			

There are 21 hits at base# 56

AlwNI CAGNNNctg 26

15: 68	16: 68	17: 68	18: 68	19: 68	20: 68
21: 68	22: 68	23: 68	24: 68	25: 68	26: 68
27: 68	28: 68	29: 68	30: 68	31: 68	32: 68
33: 68	34: 68	35: 68	36: 68	39: 46	40: 46
41: 46	42: 46				

There are 22 hits at base# 68

Table 255: Analysis of frequency of matching REaptors in actual V genes

A: HpyCHAV in HC at bases 35-56

Id	Ntot	Number of mismatches..... Number										Id	Probe
		0	1	2	3	4	5	6	7	8	9	10	Cut
5	510	5	11	274	92	61	25	22	11	1	3	5	443
													6-1
													agttctcccTGCAgctgaactc
	192	54	42	32	24	15	2	3	10	3	1	6	167
													3-11
													cactgtatcTGCAaatgaacag
	58	19	7	17	6	5	1	0	1	0	2	0	54
													3-09
													ccctgtatcTGCAaatgaacag
	267	42	33	9	8	8	82	43	22	8	11	1	100
													5-51
													ccgcctaccTGCAgtggagcag
	250	111	59	41	24	7	5	1	0	0	2	0	242
													3-15
													cgctgtatcTGCAaatgaacag
10	7	0	2	0	1	0	0	0	0	0	4	0	3
													7-4.1
													cgccatatcTGCAgatctgcag
	7	0	2	2	0	0	2	1	0	0	0	0	4
													3-73
													cgccgtatcTGCAaatgaacag
	26	10	4	1	3	1	2	1	3	1	0	0	19
													5-a
													ctgcctaccTGCAgtggagcag
	21	8	2	3	1	6	1	0	0	0	0	0	20
													3-49
													tcgcctatcTGCAaatgaacag
15	1338	249	162	379	149	103	120	71	47	13	23	12	1052
	249	411	790	939	1162	1280	1316						
					1042	1233	1293	1338					

Id	Probe	dotted probe
6-1	agttctcccTGCAgctgaactc	agttctcccTGCAgctgaactc
3-11	cactgtatcTGCAaatgaacag	cac.g.at.....aa.....ag
3-09	ccctgtatcTGCAaatgaacag	ccc.g.at.....aa.....ag
5-51	ccgcctaccTGCAgtggagcag	ccgc..a.....tg..g.ag
3-15	cgctgtatcTGCAaatgaacag	c.c.g.at.....aa.....ag
7-4.1	cgccatatcTGCAgatctgcag	c.gca.at.....a.ctg.ag
3-73	cgccgtatcTGCAaatgaacag	c.gcg.at.....aa.....ag
5-a	ctgcctaccTGCAgtggagcag	ctgc..a.....tg..g.ag
3-49	tcgcctatcTGCAaatgaacag	tcgc..at.....aa.....ag

Seqs with the expected RE site only.....1004
(Counts only cases with 4 or fewer mismatches)
Seqs with only an unexpected site..... 0
Seqs with both expected and unexpected.... 48
5 (Counts only cases with 4 or fewer mismatches)
Seqs with no sites..... 0

B: B1pI in HC

	Id	Ntot	0	1	2	3	4	5	6	7	8	Ncut	Name
10	1	133	73	16	11	13	6	9	1	4	0	119	1-58 acatggaGCTGAGCagcctgag
	2	14	11	1	0	0	0	0	1	0	1	12	1-02 acatggagctgagcaggctgag
	3	34	17	8	2	6	1	0	0	0	0	0	1-18 acatggagctgaggagcctgag
	4	120	50	32	16	10	9	1	1	1	0	2	5-51 acctgcagtggagcagcctgaa
	5	55	13	11	10	17	3	1	0	0	0	0	3-15 atctgcaaatgaacagcctgaa
15	6	340	186	88	41	15	6	3	0	1	0	0	3303 atctgcaaatgaacagcctgag
	7	82	25	16	25	12	1	3	0	0	0	0	3-20 atctgcaaatgaacagtctgag
	8	3	0	2	0	1	0	0	0	0	0	0	74.1 atctgcagatctgcagcctaaa
	9	23	18	2	2	1	0	0	0	0	0	0	3-66 atcttcaaatgaacagcctgag
	10	2	1	0	1	0	0	0	0	0	0	0	3-64 atcttcaaatgggcagcctgag
20	11	486	249	78	81	38	21	10	4	4	1	467	4301 ccctgaagctgagctctgtgac
	12	16	6	3	1	0	1	1	3	1	0	1	6-1 ccctgcagctgaactctgtgac
	13	28	15	8	2	2	1	0	0	0	0	0	2-70 tccttacaatgaccaacatgga
	14	2	0	2	0	0	0	0	0	0	0	0	2-26 tccttaccatgaccacaacatgga
													601

Name	Full sequence	Dot mode
1-58	acatggaGCTGAGCagcctgag	acatggaGCTGAGCagcctgag
1-02	acatgga gctgagc aggctgagg.....
1-18	acatggagctgaggagcctgagg.....
5-51	acctgcagtggagcagcctgaa	.c..c..tg.....a
3-15	atctgcaaatgaacagcctgaa	.tc..c.aa...a.....a
3-30.3	atctgcaaatgaacagcctgag	.tc..c.aa...a.....
3-20	atctgcaaatgaacagtctgag	.tc..c.aa...a...t.....
7-4.1	atctgcagatctgcagcctaaa	.tc..c...a.ct.....a.a
3-66	atcttcaaatgaacagcctgag	.tc.tc.aa...a.....
3-64	atcttcaaatggcagcctgag	.tc.tc.aa...g.....
4-30.1	ccctgaagctgagctctgtgac	c.c.a.....tctg...c
6-1	ccctgcagctgaactctgtgac	c.c.c.....a.tctg...c
2-70	tccttacaatgaccaacatgga	t.c.tacaa...c..a..ga
2-26	tccttaccatgaccaacatgga	t.c.tacca...c..a..ga

Seqs with the expected RE site only..... 597 (counting sequences with 4 or fewer mismatches)
Seqs with only an unexpected site..... 2
Seqs with both expected and unexpected.... 2
Seqs with no sites..... 686

C: HpyCH4III, Bst4CI, or Taal in HC

In scoring whether the RE site of interest is present, only ONs that have 4 or fewer mismatches are counted.

Number of sequences..... 1617

5

10

15

20

25

Id	Ntot	0	1	2	3	4	5	6	7	8	Ncut	acngt	acngt
1	244	78	92	43	18	10	1	2	0	0	241	102#1,1	ccgtgtattACTGgcgagaga
2	457	69	150	115	66	34	11	8	3	1	434	103#2,3	ctgtgtattactgtgcgagaga
3	173	52	45	36	22	14	3	0	0	1	169	108#3	ccgtgtattactgtgcgagagg
4	16	0	3	2	2	1	6	0	1	1	8	124#5,1	ccgtgtattactgtgcaacaga
5	4	0	0	1	0	1	1	0	1	0	2	145#6	ccatgtattactgtgcaagata
6	15	1	0	1	0	6	4	1	1	1	8	158#8	ccgtgtattactgtgcgcgaga
7	23	4	8	5	2	2	1	1	0	0	21	205#12	ccacatattactgtgcacacag
8	9	1	1	1	0	3	2	1	0	0	6	226#13	ccacatattactgtgcacggat
9	7	1	3	1	1	0	0	1	0	0	6	270#14	ccacgtattactgtgcacggat
10	23	7	3	5	5	2	1	0	0	0	22	309#16,	ccttgtattactgtgcaaaaga
11	35	5	10	7	6	3	3	0	1	0	31	313#18,	ctgtgtattactgtgcaagaga
12	18	2	3	2	2	6	1	0	2	0	15	315#19	ccgtgtattactgtaccacaga
13	3	1	2	0	0	0	0	0	0	0	3	320#20	ccttgtatcactgtgcgagaga
14	117	29	23	28	22	8	4	2	1	0	110	323#22	ccgtgtattactgtgcgaaaga
15	75	21	25	13	9	1	4	2	0	0	69	330#23,	ctgtgtattactgtgcgaaaga
16	14	2	2	2	3	0	3	1	1	0	9	349#29	ccgtgtattactgtactagaga
17	2	0	0	1	0	0	1	0	0	0	1	372#33	ccgtgtattactgtgctagaga
18	1	0	0	1	0	0	0	0	0	0	1	373#34	ccgtgtattactgtactagaca
19	2	0	0	0	0	0	0	0	0	2	0	3d#36	ctgtgtattactgtgaagaaaga
20	34	4	9	9	4	5	3	0	0	0	31	428#38	ccgtgtattactgtgcgagaaa
21	17	5	4	2	2	3	1	0	0	0	16	4302#40	ccgtgtattactgtgccagaga
22	75	15	17	24	7	10	1	1	0	0	73	439#44	ctgtgtattactgtgcgagaca
23	40	14	15	4	5	1	0	1	0	0	39	551#48	ccatgtattactgtgcgagaca
24	213	26	56	60	42	20	7	2	0	0	204	5a#49	ccatgtattactgtgcgagaaa
25	Group	337	471	363	218	130	58	23	11	6			AA
	Cumulative	337	808	1171	1389	1519	1577	1600	1611	1617			

Seqs with the expected RE site only.....1511

Seqs with only an unexpected site..... 0

Table 255 D

Seqs with both expected and unexpected.... 8
 Seqs with no sites..... 0

Analysis repeated using only 8 best REadaptors

5	Id	Ntot	0	1	2	3	4	5	6	7	8+		
	1	301	78	101	54	32	16	9	10	1	0	281	102#1 ccgtgtattactgtgcgagaga
	2	493	69	155	125	73	37	14	11	3	6	459	103#2 ctgtgtattactgtgcgagaga
	3	189	52	45	38	23	18	5	4	1	3	176	108#3 ccgtgtattactgtgcgagagg
	4	127	29	23	28	24	10	6	5	2	0	114	323#22 ccgtatattactgtgcgaaaga
10	5	78	21	25	14	11	1	4	2	0	0	72	330#23 ctgtgtattactgtgcgaaaga
	6	79	15	17	25	8	11	1	2	0	0	76	439#44 ctgtgtattactgtgcgagaca
	7	43	14	15	5	5	3	0	1	0	0	42	551#48 ccatgtattactgtgcgagaca
	8	307	26	63	72	51	38	24	14	13	6	250	5a#49 ccatgtattactgtgcgaga
	1	102#1	ccgtgtattactgtgcgagaga				ccgtgtattactgtgcgagaga						
15	2	103#2	ctgtgtattactgtgcgagaga				.t.....						
	3	108#3	ccgtgtattactgtgcgagagg			g						
	4	323#22	ccgtatattactgtgcgaaaga			a.....a...						
	5	330#23	ctgtgtattactgtgcgaaaga				.t.....a...						
	6	439#44	ctgtgtattactgtgcgagaca				.t.....c.						
20	7	551#48	ccatgtattactgtgcgagaca				..a.....c.						
	8	5a#49	ccatgtattactgtgcgagaAA				..a.....AA						

Seqs with the expected RE site only.....1463 / 1617

Seqs with only an unexpected site..... 0

25 Seqs with both expected and unexpected.... 7

Seqs with no sites..... 0

Table 300: Kappa FR1 GLGs

	!	1	2	3	4	5	6	7	8	9	10	11	12	
		GAC	ATC	CAG	ATG	ACC	CAG	TCT	CCA	TCC	TCC	CTG	TCT	
	!	13	14	15	16	17	18	19	20	21	22	23		
5		GCA	TCT	GTA	GGA	GAC	AGA	GTC	ACC	ATC	ACT	TGC	!	O12
		GAC	ATC	CAG	ATG	ACC	CAG	TCT	CCA	TCC	TCC	CTG	TCT	
		GCA	TCT	GTA	GGA	GAC	AGA	GTC	ACC	ATC	ACT	TGC	!	O2
		GAC	ATC	CAG	ATG	ACC	CAG	TCT	CCA	TCC	TCC	CTG	TCT	
10		GCA	TCT	GTA	GGA	GAC	AGA	GTC	ACC	ATC	ACT	TGC	!	O18
		GAC	ATC	CAG	ATG	ACC	CAG	TCT	CCA	TCC	TCC	CTG	TCT	
		GCA	TCT	GTA	GGA	GAC	AGA	GTC	ACC	ATC	ACT	TGC	!	O8
		GAC	ATC	CAG	ATG	ACC	CAG	TCT	CCA	TCC	TCC	CTG	TCT	
15		GCA	TCT	GTA	GGA	GAC	AGA	GTC	ACC	ATC	ACT	TGC	!	A20
		GAC	ATC	CAG	ATG	ACC	CAG	TCT	CCA	TCC	TCC	CTG	TCT	
		GCA	TCT	GTA	GGA	GAC	AGA	GTC	ACC	ATC	ACT	TGC	!	A30
		AAC	ATC	CAG	ATG	ACC	CAG	TCT	CCA	TCT	GCC	ATG	TCT	
20		GCA	TCT	GTA	GGA	GAC	AGA	GTC	ACC	ATC	ACT	TGT	!	L14
		GAC	ATC	CAG	ATG	ACC	CAG	TCT	CCA	TCC	TCA	CTG	TCT	
		GCA	TCT	GTA	GGA	GAC	AGA	GTC	ACC	ATC	ACT	TGT	!	L1
		GAC	ATC	CAG	ATG	ACC	CAG	TCT	CCA	TCC	TCA	CTG	TCT	
25		GCA	TCT	GTA	GGA	GAC	AGA	GTC	ACC	ATC	ACT	TGT	!	L15
		GCC	ATC	CAG	TTG	ACC	CAG	TCT	CCA	TCC	TCC	CTG	TCT	
		GCA	TCT	GTA	GGA	GAC	AGA	GTC	ACC	ATC	ACT	TGC	!	L4
		GCC	ATC	CAG	TTG	ACC	CAG	TCT	CCA	TCC	TCC	CTG	TCT	
30		GCA	TCT	GTA	GGA	GAC	AGA	GTC	ACC	ATC	ACT	TGC	!	L18
		GAC	ATC	CAG	ATG	ACC	CAG	TCT	CCA	TCT	TCC	GTG	TCT	
		GCA	TCT	GTA	GGA	GAC	AGA	GTC	ACC	ATC	ACT	TGT	!	L5
		GAC	ATC	CAG	ATG	ACC	CAG	TCT	CCA	TCT	TCT	GTG	TCT	
35		GCA	TCT	GTA	GGA	GAC	AGA	GTC	ACC	ATC	ACT	TGT	!	L19
		GAC	ATC	CAG	TTG	ACC	CAG	TCT	CCA	TCC	TTC	CTG	TCT	
		GCA	TCT	GTA	GGA	GAC	AGA	GTC	ACC	ATC	ACT	TGC	!	L8
		GCC	ATC	CGG	ATG	ACC	CAG	TCT	CCA	TTC	TCC	CTG	TCT	
40		GCA	TCT	GTA	GGA	GAC	AGA	GTC	ACC	ATC	ACT	TGC	!	L23
		GCC	ATC	CGG	ATG	ACC	CAG	TCT	CCA	TCC	TCA	TTC	TCT	
		GCA	TCT	ACA	GGA	GAC	AGA	GTC	ACC	ATC	ACT	TGT	!	L9
		GTC	ATC	TGG	ATG	ACC	CAG	TCT	CCA	TCC	TTA	CTC	TCT	

	GCA TCT ACA GGA GAC AGA GTC ACC ATC AGT TGT !	L24
	GCC ATC CAG ATG ACC CAG TCT CCA TCC TCC CTG TCT	
	GCA TCT GTA GGA GAC AGA GTC ACC ATC ACT TGC !	L11
	GAC ATC CAG ATG ACC CAG TCT CCT TCC ACC CTG TCT	
5	GCA TCT GTA GGA GAC AGA GTC ACC ATC ACT TGC !	L12
	GAT ATT GTG ATG ACC CAG ACT CCA CTC TCC CTG CCC	
	GTC ACC CCT GGA GAG CCG GCC TCC ATC TCC TGC !	O11
	GAT ATT GTG ATG ACC CAG ACT CCA CTC TCC CTG CCC	
	GTC ACC CCT GGA GAG CCG GCC TCC ATC TCC TGC !	O1
10	GAT GTT GTG ATG ACT CAG TCT CCA CTC TCC CTG CCC	
	GTC ACC CTT GGA CAG CCG GCC TCC ATC TCC TGC !	A17
	GAT GTT GTG ATG ACT CAG TCT CCA CTC TCC CTG CCC	
	GTC ACC CTT GGA CAG CCG GCC TCC ATC TCC TGC !	A1
	GAT ATT GTG ATG ACC CAG ACT CCA CTC TCT CTG TCC	
15	GTC ACC CCT GGA CAG CCG GCC TCC ATC TCC TGC !	A18
	GAT ATT GTG ATG ACC CAG ACT CCA CTC TCT CTG TCC	
	GTC ACC CCT GGA CAG CCG GCC TCC ATC TCC TGC !	A2
	GAT ATT GTG ATG ACT CAG TCT CCA CTC TCC CTG CCC	
	GTC ACC CCT GGA GAG CCG GCC TCC ATC TCC TGC !	A19
20	GAT ATT GTG ATG ACT CAG TCT CCA CTC TCC CTG CCC	
	GTC ACC CCT GGA GAG CCG GCC TCC ATC TCC TGC !	A3
	GAT ATT GTG ATG ACC CAG ACT CCA CTC TCC TCA CCT	
	GTC ACC CTT GGA CAG CCG GCC TCC ATC TCC TGC !	A23
	GAA ATT GTG TTG ACG CAG TCT CCA GGC ACC CTG TCT	
25	TTG TCT CCA GGG GAA AGA GCC ACC CTC TCC TGC !	A27
	GAA ATT GTG TTG ACG CAG TCT CCA GCC ACC CTG TCT	
	TTG TCT CCA GGG GAA AGA GCC ACC CTC TCC TGC !	A11
	GAA ATA GTG ATG ACG CAG TCT CCA GCC ACC CTG TCT	
	GTG TCT CCA GGG GAA AGA GCC ACC CTC TCC TGC !	L2
30	GAA ATA GTG ATG ACG CAG TCT CCA GCC ACC CTG TCT	
	GTG TCT CCA GGG GAA AGA GCC ACC CTC TCC TGC !	L16
	GAA ATT GTG TTG ACA CAG TCT CCA GCC ACC CTG TCT	
	TTG TCT CCA GGG GAA AGA GCC ACC CTC TCC TGC !	L6
	GAA ATT GTG TTG ACA CAG TCT CCA GCC ACC CTG TCT	
35	TTG TCT CCA GGG GAA AGA GCC ACC CTC TCC TGC !	L20
	GAA ATT GTA ATG ACA CAG TCT CCA GCC ACC CTG TCT	

	TTG TCT CCA GGG GAA AGA GCC ACC CTC TCC TGC !	L25
	GAC ATC GTG ATG ACC CAG TCT CCA GAC TCC CTG GCT	
	GTG TCT CTG GGC GAG AGG GCC ACC ATC AAC TGC !	B3
	GAA ACG ACA CTC ACG CAG TCT CCA GCA TTC ATG TCA	
5	GCG ACT CCA GGA GAC AAA GTC AAC ATC TCC TGC !	B2
	GAA ATT GTG CTG ACT CAG TCT CCA GAC TTT CAG TCT	
	GTG ACT CCA AAG GAG AAA GTC ACC ATC ACC TGC !	A26
	GAA ATT GTG CTG ACT CAG TCT CCA GAC TTT CAG TCT	
	GTG ACT CCA AAG GAG AAA GTC ACC ATC ACC TGC !	A10
10	GAT GTT GTG ATG ACA CAG TCT CCA GCT TTC CTC TCT	
	GTG ACT CCA GGG GAG AAA GTC ACC ATC ACC TGC !	A14

Table 302 RERS sites found in Human Kappa FR1 GLGs

	MslI	FokI --> <-- <-->	PflFI	BsrI	BsmAI	MnlI	HpyCH 4V
VKI							
O12 1-69	3	3 23	12 49	15	18 47	25	36
O2 101-169	103	103 123	112 149	115	118 147	126	136
O18 201-269	203	203 223	212 249	215	218 247	226	236
O8 301-369	303	303 323	312 349	315	318 347	326	336
A20 401-469	403	403 423	412 449	415	418 447	426	436
A30 501-569	503	503 523	512 549	515	518 547	526	536
L14 601-669	603	603	612 649	615	618 647	-	636
L1 701-769	703	703 723	712 749	715	718 747	726	736
L15 801-869	803	803 823	812 849	815	818 847	826	836
L4 901-969	-	903 923	912 949	906 915	918 947	926	936
L18 1001-1069	-	1003	1012 1049	1006 1015	1018 1047	1026	1036
L5 1101-1169	1103	-	1112 1149	1115	1118 1147	-	1136
L19 1201-1269	1203	1203	1212 1249	1215	1218 1247	-	1236
L8 1301-1369	-	1303 1323	1312 1349	1306 1315	1318 1347	-	1336
L23 1401-1469	1403	1403 1408	1412 1449	1415	1418 1447	-	1436
L9 1501-1569	1503	1503 1508 1523	1512 1549	1515	1518 1547	1526	1536
L24 1601-1669	1603	1608 1623	1612 1649	1615	1618 1647	-	1636
L11 1701-1769	1703	1703 1723	1712 1749	1715	1718 1747	1726	1736
L12 1801-1869	1803	1803	1812 1849	1815	1818 1847	-	1836

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	MslI	FokI --> <--> -->	PflPI	BsrI	BsmAI	MnlI	HpyCH 4V
VKII							
O11 1901-1969	-	-	-	-	-	1956	-
O1 2001-2069	-	-	-	-		2056	-
A17 2101-2169	-	-	2112	-	2118	2156	-
A1 2201-2269	-	-	2212	-	2218	2256	-
A18 2301-2369	-	-	-	-	-	2356	-
A2 2401-2469	-	-	-	-	-	2456	-
A19 2501-2569	-	-	2512	-	2518	2556	-
A3 2601-2669	-	-	2612	-	2618	2656	-
A23 2701-2769	-	-	-	-	-	2729 2756	-
VKIII							
A27 2801-2869	-	-	2812	-	2818 2839	2860	-
A11 2901-2969	-	-	2912	-	2918 2939	2960	-
L2 3001-3069	-	-	3012	-	3018 3039	3060	-
L16 3101-3169	-	-	3112	-	3118 3139	3160	-
L6 3201-3269	-	-	3212	-	3218 3239	3260	-

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	MslI	FokI --> <---	PflFI	BsrI	BsmAI	MnlI	HpyCH 4V
L20 3301-3369	-	-	3312	-	3318 3339	3360	-
L25 3401-3469	-	-	3412	-	3418 3439	3460	-
VRIV							
B3 3501-3569	3503	-	3512	3515	3518 3539	3551<	-
URV							
B2 3601-3669	-	-	3649	-	3618 3647	-	-
URVI							
A26 3701-3769	-	-	3712	-	3718	-	-
A10 3801-3869	-	-	3812	-	3818	-	-
A14 3901-3969	-	-	3912	-	3918	3930>	-

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Table 302 RERS sites found in Human Kappa FR1 GLGs, continued

	SfaNI	SfcI	HinfI	MlyI --> -->	MaeIII Tsp45I same sites	HphI xx38 xx56 xx62	HpaII MspI xx06 xx52
VRKI							
O12 1-69	37	41	53	53	55	56	-
O2 101-169	137	141	153	153	155	156	-
O18 201-269	237	241	253	253	255	256	-

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	SfaNI	SfcI	HinfI	MlyI --> --> <--	MaeIII Tsp45I same sites	HphI xx38 xx56 xx62	HpaII MspI xx06 xx52
O8 301-369	337	341	353	353	355	356	-
A20 401-469	437	441	453	453	455	456	-
A30 501-569	537	541	553	553	555	556	-
L14 601-669	637	641	653	653	655	656	-
L1 701-769	737	741	753	753	755	756	-
L15 801-869	837	841	853	853	855	856	-
L4 901-969	937	941	953	953	955	956	-
L18 1001-1069	1037	1041	1053	1053	1055	1056	-
L5 1101-1169	1137	1141	1153	1153	1155	1156	-
L19 1201-1269	1237	1241	1253	1253	1255	1256	-
L8 1301-1369	1337	1341	1353	1353	1355	1356	-
L23 1401-1469	1437	1441	1453	1453	1455	1456	1406
L9 1501-1569	1537	1541	1553	1553	1555	1556	1506
L24 1601-1669	1637	1641	1653	1653	1655	1656	
L11 1701-1769	1737	1741	1753	1753	1755	1756	
L12 1801-1869	1837	1841	1853	1853	1855	1856	
UNK1							
O11 1901-1969	-	-	1918	1918	1937	1938	1952
O1 2001-2069	-	-	2018	2018	2037	2038	2052
A17 2101-2169	-	-	2112	2112	2137	2138	2152
A1 2201-2269	-	-	2212	2212	2237	2238	2252

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	SfaNI	SfcI	HinfI	MlyI --> --> <--	MaeIII Tsp45I same sites	HphI xx38 xx56 xx62	HpaII MspI xx06 xx52
A18 2301-2369	-	-	2318	2318	2337	2338	2352
A2 2401-2469	-	-	2418	2418	2437	2438	2452
A19 2501-2569	-	-	2512	2512	2537	2538	2552
A3 2601-2669	-	-	2612	2612	2637	2638	2652
A23 2701-2769	-	-	2718	2718	2737	2731* 2738*	-
VRIII							
A27 2801-2869	-	-	-	-			-
A11 2901-2969	-	-	-	-			-
L2 3001-3069	-	-	-	-			-
L16 3101-3169	-	-	-	-			-
L6 3201-3269	-	-	-	-			-
L20 3301-3369	-	-	-	-			-
L25 3401-3469	-	-	-	-			-
VRIV							
B3 3501-3569	-	-	3525	3525			-
VRV							
B2 3601-3669	-	-	3639	3639			-
VRVI							
A26 3701-3769	-	-	3712	3712	3737 3755	3756 3762	-
A10 3801-3869	-	-	3812	3812	3837 3855	3856 3862	-
A14 3901-3969	-	-	3939	3939	3937 3955	3956 3962	-

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MISSING AT THE TIME OF PUBLICATION

Table 302 RERS sites found in Human Kappa FR1, continued

	BsaJI xx29 xx42 xx43 I	BssKI (NstNI) xx22 xx30 xx43	BpmI xx20 xx41 xx44 --> --> <--	BsrFI Cac8I NaeI NgoMI V	HaeII I	Tsp509I
VKI						
O12 1-69	-	-	-	-	-	-
O2 101-169	-	-	-	-	-	-
O18 201-269	-	-	-	-	-	-
O8 301-369	-	-	-	-	-	-
A20 401-469	-	-	-	-	-	-
A30 501-569	-	-	-	-	-	-
L14 601-669	-	-	-	-	-	-
L1 701-769	-	-	-	-	-	-
L15 801-869	-	-	-	-	-	-
L4 901-969	-	-	-	-	-	-
L18 1001-1069	-	-	-	-	-	-
L5 1101-1169	-	-	-	-	-	-
L19 1201-1269	-	-	-	-	-	-
L8 1301-1369	-	-	-	-	-	-
L23 1401-1469	-	-	-	-	-	-
L9 1501-1569	-	-	-	-	-	-
L24 1601-1669	-	-	-	-	-	-

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	BsaJI xx29 xx42 xx43	BssKI (NstNI) xx22 xx30 xx43	BpmI xx20 xx41 xx44 --> --> <--	BsrFI Cac8I NaeI NgoMI V	HaeII I	Tsp509I
L11 1701-1769	-	-	-	-	-	-
L12 1801-1869	-	-	-	-	-	-
VRKII						
O11 1901-1969	1942	1943	1944	1951	1954	-
O1 2001-2069	2042	2043	2044	2051	2054	-
A17 2101-2169	2142	-	-	2151	2154	-
A1 2201-2269	2242	-	-	2251	2254	-
A18 2301-2369	2342	2343	-	2351	2354	-
A2 2401-2469	2442	2443	-	2451	2454	-
A19 2501-2569	2542	2543	2544	2551	2554	-
A3 2601-2669	2642	2643	2644	2651	2654	-
A23 2701-2769	2742	-	-	2751	2754	-
VRKII						
A27 2801-2869	2843	2822 2843	2820 2841	-	-	2803
A11 2901-2969	2943	2943	2920 2941	-	-	2903
L2 3001-3069	3043	3043	3041	-	-	-
L16 3101-3169	3143	3143	3120 3141	-	-	-
L6 3201-3269	3243	3243	3220 3241	-	-	3203
L20 3301-3369	3343	3343	3320 3341	-	-	3303

	BsaJI xx29 xx42 xx43	BssKI (NstNI) xx22 xx30 xx43	BpmI xx20 xx41 xx44 --> --> <--	BsrFI Cac8I NaeI NgomI V	HaeII I	Tsp509I
L25 3401-3469	3443	3443	3420 3441	-	-	3403
VRIV						
B3 3501-3569	3529	3530	3520	-	3554	
VRV						
B2 3601-3669		3643	3620 3641	-	-	
VRVI						
A26 3701-3769		-	3720	-	-	3703
A10 3801-3869		-	3820	-	-	3803
A14 3901-3969	3943	3943	3920 3941	-	-	-

Table 400 Lambda FR1 GLG sequences

! VL1

5 CAG TCT GTG CTG ACT CAG CCA CCC TCG GTG TCT GAA
 GCC CCC AGG CAG AGG GTC ACC ATC TCC TGT ! 1a
 cag tct gtg ctg acG cag ccG ccc tcA gtg tct gGG
 gcc ccA Ggg cag agg gtc acc atc tcc tgC ! 1e
 cag tct gtg ctg act cag cca ccc tcA gCg tct gGG
 Acc ccc Ggg cag agg gtc acc atc tcT tgt ! 1c
 cag tct gtg ctg act cag cca ccc tcA gCg tct gGG
 10 Acc ccc Ggg cag agg gtc acc atc tcT tgt ! 1g
 cag tct gtg Ttg acG cag ccG ccc tcA gtg tct gCG
 gcc ccA GgA cag aAg gtc acc atc tcc tgC ! 1b

! VL2

15 CAG TCT GCC CTG ACT CAG CCT CCC TCC GCG TCC GGG
 TCT CCT GGA CAG TCA GTC ACC ATC TCC TGC ! 2c
 cag tct gcc ctg act cag cct cGc tcA gTg tcc ggg
 tct cct gga cag tca gtc acc atc tcc tgc ! 2e
 cag tct gcc ctg act cag cct Gcc tcc gTg tcT ggg
 tct cct gga cag tcG Atc acc atc tcc tgc ! 2a2
 20 cag tct gcc ctg act cag cct ccc tcc gTg tcc ggg
 tct cct gga cag tca gtc acc atc tcc tgc ! 2d
 cag tct gcc ctg act cag cct Gcc tcc gTg tcT ggg
 tct cct gga cag tcG Atc acc atc tcc tgc ! 2b2

! VL3

25 TCC TAT GAG CTG ACT CAG CCA CCC TCA GTG TCC GTG
 TCC CCA GGA CAG ACA GCC AGC ATC ACC TGC ! 3r
 tcc tat gag ctg act cag cca cTc tca gtg tcA gtg
 Gcc cTG gga cag acG gcc agG atT acc tgT ! 3j
 tcc tat gag ctg acA cag cca ccc tcG gtg tcA gtg
 30 tcc cca gga caA acG gcc agG atc acc tgc ! 3p
 tcc tat gag ctg acA cag cca ccc tcG gtg tcA gtg
 tcc cTa gga cag aTG gcc agG atc acc tgc ! 3a
 tcT tCt gag ctg act cag GAC ccT GcT gtg tcT gtg
 Gcc TTG gga cag aca gTc agG atc acA tgc ! 3l

tcc tat gTg ctg act cag cca ccc tca gtg tcA gtg
 Gcc cca gga Aag acG gcc agG atT acc tgT ! 3h
 tcc tat gag ctg acA cag cTa ccc tcG gtg tcA gtg
 tcc cca gga cag aca gcc agG atc acc tgc ! 3e
 5 tcc tat gag ctg aTG cag cca ccc tcG gtg tcA gtg
 tcc cca gga cag acG gcc agG atc acc tgc ! 3m
 tcc tat gag ctg acA cag cca Tcc tca gtg tcA gtg
 tcT ccG gga cag aca gcc agG atc acc tgc ! V2-19
 ! VL4
 10 CTG CCT GTG CTG ACT CAG CCC CCG TCT GCA TCT GCC
 TTG CTG GGA GCC TCG ATC AAG CTC ACC TGC ! 4c
 cAg cct gtg ctg act caA TcA TcC tct gcC tct gct
 tCC ctg gga Tcc tcg Gtc aag ctc acc tgc ! 4a
 cAg cTt gtg ctg act caA TcG ccC tct gcC tct gcc
 15 tCC ctg gga gcc tcg Gtc aag ctc acc tgc ! 4b
 ! VL5
 CAG CCT GTG CTG ACT CAG CCA CCT TCC TCC TCC GCA
 TCT CCT GGA GAA TCC GCC AGA CTC ACC TGC ! 5e
 cag Gct gtg ctg act cag ccG Gct tcc CTc tcT gca
 20 tct cct gga gCa tcA gcc agT ctc acc tgc ! 5c
 cag cct gtg ctg act cag cca Tct tcc CAT tcT gca
 tct Tct gga gCa tcA gTc aga ctc acc tgc ! 5b
 ! VL6
 AAT TTT ATG CTG ACT CAG CCC CAC TCT GTG TCG GAG
 25 TCT CCG GGG AAG ACG GTA ACC ATC TCC TGC ! 6a
 ! VL7
 CAG ACT GTG GTG ACT CAG GAG CCC TCA CTG ACT GTG
 TCC CCA GGA GGG ACA GTC ACT CTC ACC TGT ! 7a
 cag Gct gtg gtg act cag gag ccc tca ctg act gtg
 30 tcc cca gga ggg aca gtc act ctc acc tgt ! 7b
 ! VL8
 CAG ACT GTG GTG ACC CAG GAG CCA TCG TTC TCA GTG
 TCC CCT GGA GGG ACA GTC ACA CTC ACT TGT ! 8a

! VL9

CAG CCT GTG CTG ACT CAG CCA CCT TCT GCA TCA GCC
TCC CTG GGA GCC TCG GTC ACA CTC ACC TGC ! 9a

! VL10

5

CAG GCA GGG CTG ACT CAG CCA CCC TCG GTG TCC AAG
GGC TTG AGA CAG ACC GCC ACA CTC ACC TGC ! 10a

Table 405 RERSs found in human lambda FR1 GLGs

! There are 31 lambda GLGs

MlyI NnnnnnGACTC

25

1: 6 3: 6 4: 6 6: 6 7: 6 8: 6
 5 9: 6 10: 6 11: 6 12: 6 15: 6 16: 6
 20: 6 21: 6 22: 6 23: 6 23: 50 24: 6
 25: 6 25: 50 26: 6 27: 6 28: 6 30: 6
 31: 6

There are 23 hits at base# 6

10

-"- GAGTCNNNNNn

1

26: 34

MwoI GCNNNNNnngc

20

15 1: 9 2: 9 3: 9 4: 9 11: 9 11: 56
 12: 9 13: 9 14: 9 16: 9 17: 9 18: 9
 19: 9 20: 9 23: 9 24: 9 25: 9 26: 9
 30: 9 31: 9

There are 19 hits at base# 9

20 HinfI Gantc

27

1: 12 3: 12 4: 12 6: 12 7: 12 8: 12
 9: 12 10: 12 11: 12 12: 12 15: 12 16: 12
 20: 12 21: 12 22: 12 23: 12 23: 46 23: 56
 24: 12 25: 12 25: 56 26: 12 26: 34 27: 12
 25 28: 12 30: 12 31: 12

There are 23 hits at base# 12

PleI gactc

25

1: 12 3: 12 4: 12 6: 12 7: 12 8: 12
 9: 12 10: 12 11: 12 12: 12 15: 12 16: 12
 30 20: 12 21: 12 22: 12 23: 12 23: 56 24: 12
 25: 12 25: 56 26: 12 27: 12 28: 12 30: 12
 31: 12

There are 23 hits at base# 12

35 -"- gagtc

1

26: 34

DdeI Ctnag 32

	1: 14	2: 24	3: 14	3: 24	4: 14	4: 24
	5: 24	6: 14	7: 14	7: 24	8: 14	9: 14
5	10: 14	11: 14	11: 24	12: 14	12: 24	15: 5
	15: 14	16: 14	16: 24	19: 24	20: 14	23: 14
	24: 14	25: 14	26: 14	27: 14	28: 14	29: 30
	30: 14	31: 14				

There are 21 hits at base# 14

10

BsaJI Ccnngg 38

	1: 23	1: 40	2: 39	2: 40	3: 39	3: 40
	4: 39	4: 40	5: 39	11: 39	12: 38	12: 39
	13: 23	13: 39	14: 23	14: 39	15: 38	16: 39
15	17: 23	17: 39	18: 23	18: 39	21: 38	21: 39
	21: 47	22: 38	22: 39	22: 47	26: 40	27: 39
	28: 39	29: 14	29: 39	30: 38	30: 39	30: 47
	31: 23	31: 32				

There are 17 hits at base# 39

20 There are 5 hits at base# 38

There are 5 hits at base# 40 Makes cleavage ragged.

MnlI cctc 35

	1: 23	2: 23	3: 23	4: 23	5: 23	6: 19
	6: 23	7: 19	8: 23	9: 19	9: 23	10: 23
25	11: 23	13: 23	14: 23	16: 23	17: 23	18: 23
	19: 23	20: 47	21: 23	21: 29	21: 47	22: 23
	22: 29	22: 35	22: 47	23: 26	23: 29	24: 27
	27: 23	28: 23	30: 35	30: 47	31: 23	

There are 21 hits at base# 23

30 There are 3 hits at base# 19

There are 3 hits at base# 29

There are 1 hits at base# 26

There are 1 hits at base# 27 These could make cleavage ragged.

-"- gagg 7

35	1: 48	2: 48	3: 48	4: 48	27: 44	28: 44
----	-------	-------	-------	-------	--------	--------

29: 44

BssKI Nccngg 39

1: 40 2: 39 3: 39 3: 40 4: 39 4: 40
 5 5: 39 6: 31 6: 39 7: 31 7: 39 8: 39
 9: 31 9: 39 10: 39 11: 39 12: 38 12: 52
 13: 39 13: 52 14: 52 16: 39 16: 52 17: 39
 17: 52 18: 39 18: 52 19: 39 19: 52 21: 38
 22: 38 23: 39 24: 39 26: 39 27: 39 28: 39
 10 29: 14 29: 39 30: 38

There are 21 hits at base# 39

There are 4 hits at base# 38

There are 3 hits at base# 31

There are 3 hits at base# 40 Ragged

15

BstNI CCwgg 30

1: 41 2: 40 5: 40 6: 40 7: 40 8: 40
 9: 40 10: 40 11: 40 12: 39 12: 53 13: 40
 13: 53 14: 53 16: 40 16: 53 17: 40 17: 53
 20 18: 40 18: 53 19: 53 21: 39 22: 39 23: 40
 24: 40 27: 40 28: 40 29: 15 29: 40 30: 39

There are 17 hits at base# 40

There are 7 hits at base# 53

There are 4 hits at base# 39

25 There are 1 hits at base# 41 Ragged

PspGI ccwgg 30

1: 41 2: 40 5: 40 6: 40 7: 40 8: 40
 9: 40 10: 40 11: 40 12: 39 12: 53 13: 40
 30 13: 53 14: 53 16: 40 16: 53 17: 40 17: 53
 18: 40 18: 53 19: 53 21: 39 22: 39 23: 40
 24: 40 27: 40 28: 40 29: 15 29: 40 30: 39

There are 17 hits at base# 40

There are 7 hits at base# 53

35 There are 4 hits at base# 39

There are 1 hits at base# 41

ScrFI CCngg

39

5 1: 41 2: 40 3: 40 3: 41 4: 40 4: 41
5: 40 6: 32 6: 40 7: 32 7: 40 8: 40
9: 32 9: 40 10: 40 11: 40 12: 39 12: 53
13: 40 13: 53 14: 53 16: 40 16: 53 17: 40
17: 53 18: 40 18: 53 19: 40 19: 53 21: 39
22: 39 23: 40 24: 40 26: 40 27: 40 28: 40
10 29: 15 29: 40 30: 39

There are 21 hits at base# 40

There are 4 hits at base# 39

There are 3 hits at base# 41

15 MaeIII gtnac

16

1: 52 2: 52 3: 52 4: 52 5: 52 6: 52
7: 52 9: 52 26: 52 27: 10 27: 52 28: 10
28: 52 29: 10 29: 52 30: 52

There are 13 hits at base# 52

20

Tsp45I gtsac

15

1: 52 2: 52 3: 52 4: 52 5: 52 6: 52
7: 52 9: 52 27: 10 27: 52 28: 10 28: 52
29: 10 29: 52 30: 52

25 There are 12 hits at base# 52

HphI tcacc

26

30 1: 53 2: 53 3: 53 4: 53 5: 53 6: 53
7: 53 8: 53 9: 53 10: 53 11: 59 13: 59
14: 59 17: 59 18: 59 19: 59 20: 59 21: 59
22: 59 23: 59 24: 59 25: 59 27: 59 28: 59
30: 59 31: 59

There are 16 hits at base# 59

There are 10 hits at base# 53

35

BspMI ACCTGCNNNNn

14

11: 61 13: 61 14: 61 17: 61 18: 61 19: 61

20: 61 21: 61 22: 61 23: 61 24: 61 25: 61

30: 61 31: 61

5 There are 14 hits at base# 61 Goes into CDR1

Table 500: h3401-h2 captured Via CJ with BsmAI

```

! 1  2  3  4  5  6  7  8  9 10 11 12 13 14 15
! S  A  Q  D  I  Q  M  T  Q  S  P  A  T  L  S
aGT GCA Caa gac atc cag atg acc cag tct cca gcc acc ctg tct
5 ! ApaLI... a gcc acc !
L25,L6,L20,L2,L16,A11
! Extender.....Bridge...

! 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30
10 ! V  S  P  G  E  R  A  T  L  S  C  R  A  S  Q
    gtg tct cca ggg gaa agg gcc acc ctg tcc tgc agg gcc agt cag

! 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45
15 ! S  V  S  N  N  L  A  W  Y  Q  Q  K  P  G  Q
    agt gtt agt aac aac tta gcc tgg tac cag cag aaa cct ggc cag

! 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60
20 ! V  P  R  L  L  I  Y  G  A  S  T  R  A  T  D
    gtt ccc agg ctg ctg atc tat ggt gca tcc acc agg gcc act gat

! 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75
! I  P  A  R  F  S  G  S  G  S  G  T  D  F  T
    atc cca gcc agg ttc agt ggc agt ggg tct ggg aca gac ttc act

25 ! 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90
    ! L  T  I  S  R  L  E  P  E  D  F  A  V  Y  Y
    ctg acc atc agc aga ctg gag cct gaa gat ttt gca gtg tat tac

30 ! 91 92 93 94 95 96 97 98 99 100 101 102 103 104 105
    ! C  Q  R  Y  G  S  S  P  G  W  T  F  G  Q  G
    tgt cag cgg tat ggt agc tca ccg ggg tgg acg ttc ggc caa ggg

! 106 107 108 109 110 111 112 113 114 115 116 117 118 119 120
35 ! T  K  V  E  I  K  R  T  V  A  A  P  S  V  F
    acc aag gtg gaa atc aaa cga act gtg gct gca cca tct gtc ttc

! 121 122 123 124 125 126 127 128 129 130 131 132 133 134 135
40 ! I  F  P  P  S  D  E  Q  L  K  S  G  T  A  S
    atc ttc ccg cca tct gat gag cag ttg aaa tct gga act gcc tct

! 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150
! V  V  C  L  L  N  N  F  Y  P  R  E  A  K  V
    gtt gtg tgc ctg ctg aat aac ttc tat ccc aga gag gcc aaa gta

```

```

! 151 152 153 154 155 156 157 158 159 160 161 162 163 164 165
!   Q   W   K   V   D   N   A   L   Q   S   G   N   S   Q   E
   cag tgg aag gtg gat aac gcc ctc caa tcg ggt aac tcc cag gag

5  ! 166 167 168 169 170 171 172 173 174 175 176 177 178 179 180
!   S   V   T   E   Q   D   S   K   D   S   T   Y   S   L   S
   agt gtc aca gag cag gac agc aag gac agc acc tac agc ctc agc

10 ! 181 182 183 184 185 186 187 188 189 190 191 192 193 194 195
!   S   T   L   T   L   S   K   A   D   Y   E   K   H   K   V
   agc acc ctg acg ctg agc aaa gca gac tac gag aaa cac aaa gtc

! 196 197 198 199 200 201 202 203 204 205 206 207 208 209 210
!   Y   A   C   E   V   T   H   Q   G   L   S   S   P   V   T
15  tac gcc tgc gaa gtc acc cat cag ggc ctg agc tcg cct gtc aca

! 211 212 213 214 215 216 217 218 219 220 221 222 223
!   K   S   F   N   K   G   E   C   K   G   E   F   A
20  aag agc ttc aac aaa gga gag tgt aag ggc gaa ttc gc.....

```

Table 501: h3401-d8 KAPPA captured with CJ and BsmAI

```

25 ! 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15
!   S   A   Q   D   I   Q   M   T   Q   S   P   A   T   L   S
   aGT GCA Caa gac atc cag atg acc cag tct cct gcc acc ctg tct
!   ApaLI...Extender.....a gcc acc !
L25,L6,L20,L2,L16,A11
!
30 !
!
! 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30
!   V   S   P   G   E   R   A   T   L   S   C   R   A   S   Q
   gtg tct cca ggt gaa aga gcc acc ctc tcc tgc agg gcc agt cag
! GTG TCT CCA GGG GAA AGA GCC ACC CTC TCC TGC ! L2
35 !
!
! 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45
!   N   L   L   S   N   L   A   W   Y   Q   Q   K   P   G   Q
   aat ctt ctc agc aac tta gcc tgg tac cag cag aaa cct ggc cag
40 !
!
! 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60
!   A   P   R   L   L   I   Y   G   A   S   T   G   A   I   G
   gct ccc agg ctc ctc atc tat ggt gct tcc acc ggg gcc att ggt
45 !
!
! 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75
!   I   P   A   R   F   S   G   S   G   S   G   T   E   F   T
   atc cca gcc agg ttc agt ggc agt ggg tct ggg aca gag ttc act

```

```

! 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90
! L T I S S L Q S E D F A V Y F
ctc acc atc agc agc ctg cag tct gaa gat ttt gca gtg tat ttc

5 ! 91 92 93 94 95 96 97 98 99 100 101 102 103 104 105
! C Q Q Y G T S P P T F G G G T
tgt cag cag tat ggt acc tca ccg ccc act ttc ggc gga ggg acc

10 ! 106 107 108 109 110 111 112 113 114 115 116 117 118 119 120
! K V E I K R T V A A P S V F I
aag gtg gag atc aaa cga act gtg gct gca cca tct gtc ttc atc

! 121 122 123 124 125 126 127 128 129 130 131 132 133 134 135
! F P P S D E Q L K S G T A S V
15 ttc ccg cca tct gat gag cag ttg aaa tct gga act gcc tct gtt

! 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150
! V C P L N N F Y P R E A K V Q
20 gtg tgc ccg ctg aat aac ttc tat ccc aga gag gcc aaa gta cag

! 151 152 153 154 155 156 157 158 159 160 161 162 163 164 165
! W K V D N A L Q S G N S Q E S
tggt aag gtg gat aac gcc ctc caa tcg ggt aac tcc cag gag agt

25 ! 166 167 168 169 170 171 172 173 174 175 176 177 178 179 180
! V T E Q D N K D S T Y S L S S
gtc aca gag cag gac aac aag gac agc acc tac agc ctc agc agc

! 181 182 183 184 185 186 187 188 189 190 191 192 193 194 195
! T L T L S K V D Y E K H E V Y
30 acc ctg acg ctg agc aaa gta gac tac gag aaa cac gaa gtc tac

! 196 197 198 199 200 201 202 203 204 205 206 207 208 209 210
! A C E V T H Q G L S S P V T K
35 gcc tgc gaa gtc acc cat cag ggc ctt agc tcg ccc gtc acg aag

! 211 212 213 214 215 216 217 218 219 220 221 222 223
! S F N R G E C K K E F V
40 agc ttc aac agg gga gag tgt aag aaa gaa ttc gtt t

```

Table 508 Human heavy chains bases 88.1 to 94.2

Number of sequences..... 840

5

10

15

20

25

30

35

Id	Ntot	0	1	2	3	4	5	6	7	Name	Sequence.....	Probe	Dot form.....
1	364	152	97	76	26	7	4	2	0	VHS881-1.1	gctgtgtattactgtgcgag	gctgtgtattactgtgcgag	gctgtgtattactgtgcgag
2	265	150	60	33	13	5	4	0	0	VHS881-1.2	gccgtgtattactgtgcgag	gccgtgtattactgtgcgag	..C.....
3	96	14	34	16	10	5	7	9	1	VHS881-2.1	gccgtattactgtgcgag	gccgtattactgtgcgag	..C..a.....
4	20	0	3	4	9	2	2	0	0	VHS881-4.1	gccgtgtattactgtgcgag	gccgtgtattactgtgcgag	..C.....a.....
5	95	25	36	18	11	2	2	0	1	VHS881-9.1	gccatgtattactgtgcgag	gccatgtattactgtgcgag	..ca.....
840 341 230 147 69 21 19 11 2													
341 571 718 787 808 827 838 840													
88 89 90 91 92 93 94 95 Codon number as in Table 195													
Recognition..... Stem..... Loop. Stem.....													
(VHS881-1.1) 5'-gtgtgtat tact-gtgcgag <u>cAcATccgTg</u> TTgTT <u>cAcggATgTg</u> -3'													
(VHS881-1.2) 5'-gccgtgtat tact-gtgcgag <u>cAcATccgTg</u> TTgTT <u>cAcggATgTg</u> -3'													
(VHS881-2.1) 5'-gccgtatat tact-gtgcgag <u>cAcATccgTg</u> TTgTT <u>cAcggATgTg</u> -3'													
(VHS881-4.1) 5'-gccgtgtat tact-gtgcgag <u>cAcATccgTg</u> TTgTT <u>cAcggATgTg</u> -3'													
(VHS881-9.1) 5'-gccatgtat tact-gtgcgag <u>cAcATccgTg</u> TTgTT <u>cAcggATgTg</u> -3'													
site of substrate cleavage													
(FOKIact)	5'	<u>cAcATccgTg</u> TTgTT <u>cAcggATgTg</u> -3'											
(VHEx881)	5'	AATAgTAGAc TgcAgTgTcc TcAgcccTTA AgcTgTTcAT cTgcAAGTAG- AgAgTATtCT TAGAgTTgTc TcTAGAcTTA gTgAAgcg-3'											
! note that VHEx881 is the reverse complement of the ON below													
[RC] 5'-cgCttcacTaag-													
Scab.....													
Synthetic 3-23 as in Table 206													
TCT AGA gac aac tct aag aat act ctc tac ttg cag atg -													
XbaI...													
aac agC TTA AGg gct gag gac aCT GCA Gtc tac tat t-3'													
AflII...													
(VHBA881)	5'	cgCttcacTaag-											
TCT AGA gac aac tct aag aat act ctc tac ttg cag atg -													
aac agC TTA AGg gct gag gac aCT GCA Gtc tac tat tgt gcg ag-3'													
(VHBB881)	5'	cgCttcacTaag-											

88 89 90 91 92 93 94 95 Codon number as in Table 195

Recognition..... Stem..... Loop. Stem.....

(VHS881-1.1) 5'-gctgtgtat|tact-gtgcgag cAcATccgTg TTgTT cAcgATgTg-3'(VHS881-1.2) 5'-gccgtgtat|tact-gtgcgag cAcATccgTg TTgTT cAcgATgTg-3'(VHS881-2.1) 5'-gccgtat|tact-gtgcgag cAcATccgTg TTgTT cAcgATgTg-3'(VHS881-4.1) 5'-gccgtgtat|tact-gtgcgag cAcATccgTg TTgTT cAcgATgTg-3'(VHS881-9.1) 5'-gccatgtat|tact-gtgcgag cAcATccgTg TTgTT cAcgATgTg-3'

| site of substrate cleavage

(FOKIact) 5'-cAcATccgTg TTgTT cAcgATgTg-3'

(VHEX881) 5'-AATAGTAGAc TgcAgTgTcc TcAgcccTTA AgcTgTtCAT cTgcAAgTAG-AgAgTATTCT TAGAgTgTc TcTAGAcTTA gTgAAgcg-3'

! note that VHEX881 is the reverse complement of the ON below

! [RC] 5'-cgCttcacTaag-

! Scab.....

! Synthetic 3-23 as in Table 206

! |TCT|AGA|gac|aac|tct|aat|act|ctc|tac|ttg|cag|atg|-

! XbaI...

! |aac|agC|TTA|AGg|gct|gag|gac|aCT|GCA|Gtc|tac|tat|t-3'

! AflII...

(VHBA881) 5'-cgCttcacTaag-

|TCT|AGA|gac|aac|tct|aat|act|ctc|tac|ttg|cag|atg|-

|aac|agC|TTA|AGg|gct|gag|gac|aCT|GCA|Gtc|tac|tat|tgt gcg ag-3'

(VHBB881) 5'-cgCttcacTaag-

|TCT|AGA|gac|aac|tct|aat|act|ctc|tac|ttg|cag|atg|
 |aac|agc|TTA|AGG|gct|gag|gac|aCT|GCA|Gtc|tac|tat|tgt|Acg|ag-3'
 (VH881PCR) 5'-cgCttcactaag|TCT|AGA|gac|aac-3'

5 Table 512: Kappa, bases 12-30

ID	NTot	0	1	2	3	4	5	6	Name	Sequence.....	Dot Form.....
1	84	40	21	20	1	2	0	0	SK12012	gacccagtcctccatctcc	gacccagtcctccatctcc
2	32	19	3	6	2	1	0	1	SK12A17	gactcagtcctccactctcc	...t.....ct....
3	26	17	8	1	0	0	0	0	SK12A27	gacgcagtcctccaggcacc	...g.....gg.a...
4	40	21	18	1	0	0	0	0	SK12A11	gacgcagtcctccaggcacc	...g.....g.a...
	182	97	50	28	3	3	0	1			
		97	147	175	178	181	181	182			

15 URE adapters:

Stem..... Loop. Stem..... Recognition.....
 (SzKB1230-O12) 5'-cAcATccgTg TTgTT cAcggATgTg ggAggATggAgAcTgggTc-3'
 [RC] 5'-gacccagtcctccatctcc cAcATccgTg AAcAA cAcggATgTg-3'
 Recognition..... Stem..... loop. Stem.....
 FokI.

20

Stem..... Loop. Stem..... Recognition.....
 (SzKB1230-A17) 5'-cAcATccgTg TTgTT cAcggATgTg ggAggATggAgAcTgAgTc-3'
 [RC] 5'-gactcagtcctccactctcc cAcATccgTg AAcAA cAcggATgTg-3'
 Recognition..... Stem..... loop. Stem.....
 FokI.

25

Stem..... Loop. Stem..... Recognition.....
 (SzKB1230-A27) 5'-cAcATccgTg TTgTT cAcggATgTg ggTgcctggAgAcTggcTc-3'
 [RC] 5'-gacgcagtcctccaggcacc cAcATccgTg AAcAA cAcggATgTg-3'
 Recognition..... Stem..... loop. Stem.....
 FokI.

30

Stem..... Loop. Stem..... Recognition.....
 (SzKB1230-A11) 5'-cAcATccgTg TTgTT cAcggATgTg ggTggcTggAgAcTggcTc-3'
 [RC] 5'-gacgcagtcctccaggcacc cAcATccgTg AAcAA cAcggATgTg-3'
 Recognition..... Stem..... loop. Stem.....
 FokI.

35

What happens in the upper strand:

(SzkB1230-O12*)

5'-gac cca gtc|tcc a-tc ctc c-3'
| Site of cleavage in substrate

5

(SzkB1230-A17*)

5'-gac tca gtc|tcc a-ct ctc c-3'

!

(SzkB1230-A27*)

5'-gac gca gtc|tcc a-gg cac c-3'

!

10 (SzkB1230-A11*)

5'-gac gca gtc|tcc a-gc cac c-3'

(kapextURE)

5'-ccTctactctTgTcAcAgTgcAcAA gAc ATc cAg-3' !sense strand
Scab.....ApaLI.

15 (kapextUREPCR)

5'-ccTctactctTgTcAcAgTg-3'
Scab.....

(kaBRO1UR)

5'-ggAggATggA cTggATgTcT TgTgcAcTgT gAcAagAgTA gAgg-3'

!

20 [RC]

5'-ccTctactctTgTcAcAgTgcAcAA gAc ATc cAg tcc a-tc ctc c-3' ON above is R.C. of this one

(kaBRO2UR)

5'-ggAggATggA cTggATgTcT TgTgcAcTgT gAcAagAgTA gAgg-3'

!

[RC]

5'-ccTctactctTgTcAcAgTgcAcAA gAc ATc cAg tcc a-ct ctc c-3' ON above is R.C. of this one

(kaBRO3UR)

5'-ggTgccTggA cTggATgTcT TgTgcAcTgT gAcAagAgTA gAgg-3'

!

[RC]

5'-ccTctactctTgTcAcAgTgcAcAA gAc ATc cAg tcc a-gg cac c-3' ON above is R.C. of this one

(kaBRO4UR)

5'-ggTggcTggA cTggATgTcT TgTgcAcTgT gAcAagAgTA gAgg-3'

!

[RC]

5'-ccTctactctTgTcAcAgTgcAcAA gAc ATc cAg tcc a-gc cac c-3' ON above is R.C. of this one

Scab.....ApaLI.

|TCT|AGA|gac|aac|tct|aat|aat|act|ctc|tac|ttg|cag|atg|-
 |aac|agC|TTA|AGg|gct|gag|gac|aCT|GCA|Gtc|tac|tat|tgt|Acg|ag-3'
 (VH881PCR) 5'-cgCttcacTaag|TCT|AGA|gac|aac|-3'

5 Table 512: Kappa, bases 12-30

!	ID	Ntot	0	1	2	3	4	5	6	Name	Sequence.....	Dot Form.....
!	1	84	40	21	20	1	2	0	0	SK12012	gacccagtcctccatccctcc	gacccagtcctccatccctcc
!	2	32	19	3	6	2	1	0	1	SK12A17	gactcagtcctccactctcc	...t.....ct.....
!	3	26	17	8	1	0	0	0	0	SK12A27	gacgcagtcctccaggcacc	...g.....gg.a...
!	4	40	21	18	1	0	0	0	0	SK12A11	gacgcagtcctccaggcacc	...g.....g.a...
!	182	97	50	28	3	3	0	1				
!	97	147	175	178	181	181	182					

15 URE adapters:

Stem..... Loop. Stem..... Recognition.....
 (SZKB1230-O12) 5'-cAcATccgTg TTgTT cAcggATgTg ggAggATgAgAcTgggTc-3'
 [RC] 5'-gacccagtcctccatccctcc cAcATccgTg AAcAA cAcggATgTg-3'
 Recognition..... Stem..... loop. Stem.....
 FokI.

20

Stem..... Loop. Stem..... Recognition.....
 (SZKB1230-A17) 5'-cAcATccgTg TTgTT cAcggATgTg ggAggATgAgAcTgAgTc-3'
 [RC] 5'-gactcagtcctccactctcc cAcATccgTg AAcAA cAcggATgTg-3'
 Recognition..... Stem..... loop. Stem.....
 FokI.

25

Stem..... Loop. Stem..... Recognition.....
 (SZKB1230-A27) 5'-cAcATccgTg TTgTT cAcggATgTg ggTgccTggAgAcTgcgTc-3'
 [RC] 5'-gacgcagtcctccaggcacc cAcATccgTg AAcAA cAcggATgTg-3'
 Recognition..... Stem..... loop. Stem.....
 FokI.

30

Stem..... Loop. Stem..... Recognition.....
 (SZKB1230-A11) 5'-cAcATccgTg TTgTT cAcggATgTg ggTgccTggAgAcTgcgTc-3'
 [RC] 5'-gacgcagtcctccaggcacc cAcATccgTg AAcAA cAcggATgTg-3'
 Recognition..... Stem..... loop. Stem.....
 FokI.

35

What happens in the upper strand:

```

(SzKB1230-O12*)
!
5 ! 5'-gac cca gtc|tcc a-tc ctc c-3'
! | Site of cleavage in substrate
(SzKB1230-A17*)
!
! 5'-gac tca gtc|tcc a-ct ctc c-3'
(SzKB1230-A27*)
!
! 5'-gac gca gtc|tcc a-gg cac c-3'
10 (SzKB1230-A11*)
!
! 5'-gac gca gtc|tcc a-gc cac c-3'

(kapextURE) 5'-ccTctactctTgTcAcAgTgcAcAA gAc ATc cAg-3' |sense strand
Scab.....ApaLI.

15 (kapextUREPCR) 5'-ccTctactctTgTcAcAgTg-3'
Scab.....

(kaBRO1UR) 5'-ggAggATggA cTggATgTct TgTgcAcTgT gAcAAgAgTA gAgg-3'
! [RC] 5'-ccTctactctTgTcAcAgTgcAcAA gAc ATc cAg tcc a-tc ctc c-3' ON above is R.C. of this one
20 (kaBRO2UR) 5'-ggAggATggA cTggATgTct TgTgcAcTgT gAcAAgAgTA gAgg-3'
! [RC] 5'-ccTctactctTgTcAcAgTgcAcAA gAc ATc cAg tcc a-ct ctc c-3' ON above is R.C. of this one
(kaBRO3UR) 5'-ggTgcccTggA cTggATgTct TgTgcAcTgT gAcAAgAgTA gAgg-3'
! [RC] 5'-ccTctactctTgTcAcAgTgcAcAA gAc ATc cAg tcc a-gg cac c-3' ON above is R.C. of this one
(kaBRO4UR) 5'-ggTgcccTggA cTggATgTct TgTgcAcTgT gAcAAgAgTA gAgg-3'
! [RC] 5'-ccTctactctTgTcAcAgTgcAcAA gAc ATc cAg tcc a-gc cac c-3' ON above is R.C. of this one
25 ! Scab.....ApaLI.

```


What happens in the top strand:

```

!
(VL133-2a2*) 5'-g tct cct g|ga cag tcg atc
5 !
(VL133-31*) 5'-g gcc ttg g|ga cag aca gtc
!
(VL133-2c*) 5'-g tct cct g|ga cag tca gtc
!
10 (VL133-1c*) 5'-g gcc cca g|gg cag agg gtc
!
! The following Extenders and Bridges all encode the AA sequence of 2a2 for
codons 1-15
!
15 (ON_LamEx133) 5'-ccTcTgAcTgAgT gca cAg -
!
!           2  3  4  5  6  7  8  9  10 11 12
!          AGt gCt TtA acC caA ccG gCt AGT gtT AGC ggT-
!
20 !
!          13 14 15
!         tcC ccG g ! 2a2
!
!           1
! (ON_LamB1-133) [RC] 5'-ccTcTgAcTgAgT gca cAg -
!
25 !
!           2  3  4  5  6  7  8  9  10 11 12
!          AGt gCt TtA acC caA ccG gCt AGT gtT AGC ggT-
!
!           13 14 15
!         tcC ccG g ga cag tcg at-3' ! 2a2
30 ! N.B. the actual seq is the
! reverse complement of the
! one shown.
!
! (ON_LamB2-133) [RC] 5'-ccTcTgAcTgAgT gca cAg -
!
35 !
!           2  3  4  5  6  7  8  9  10 11 12
!          AGt gCt TtA acC caA ccG gCt AGT gtT AGC ggT-
!
!           13 14 15
!         tcC ccG g ga cag aca gt-3' ! 31
40 ! N.B. the actual seq is the
! reverse complement of the
! one shown.
!
! (ON_LamB3-133) [RC] 5'-ccTcTgAcTgAgT gca cAg -
45 !
!           2  3  4  5  6  7  8  9  10 11 12
!          AGt gCt TtA acC caA ccG gCt AGT gtT AGC ggT-
!
!           13 14 15
!         tcC ccG g ga cag tca gt -3' ! 2c
50 ! N.B. the actual seq is the
! reverse complement of the
! one shown.
!
! (ON_LamB4-133) [RC] 5'-ccTcTgAcTgAgT gca cAg -
55 !

```

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!           2   3   4   5   6   7   8   9   10  11  12
          AGt gcT TtA acC caA ccG gcT AGT gtT AGC ggT-
!
!           13  14  15
5         tcC ccG g gg cag agg gt-3' ! 1c  N.B. the actual seq is the
! reverse complement of the
! one shown.
!
(ON_Lam133PCR)  5'-ccTcTgAcTgAgT gcA cAg AGt gc-3'

```

Table 525 ONs used in Capture of kappa light chains using CJ method and *BsmAI*

All ONs are written 5' to 3'.

5	REdapters (6)	
	ON_20SK15O12	gggAggATggAgAcTgggTc
	ON_20SK15L12	gggAAgATggAgAcTgggTc
	ON_20SK15A17	gggAgAgTggAgAcTgAgTc
	ON_20SK15A27	gggTgccTggAgAcTgcgTc
10	ON_20SK15A11	gggTggcTggAgAcTgcgTc
	ON_20SK15B3	gggAgTcTggAgAcTgggTc
Bridges (6)		
15	kapbr11012	gggAggATggAgAcTgggTcATcTggATgTcTTgTgcAcTgTgAcAgAgg
	kapbr11L12	gggAAGATggAgAcTgggTcATcTggATgTcTTgTgcAcTgTgAcAgAgg
	kapbr11A17	gggAgAgTggAgAcTgggTcATcTggATgTcTTgTgcAcTgTgAcAgAgg
	kapbr11A27	gggTgccTggAgAcTgggTcATcTggATgTcTTgTgcAcTgTgAcAgAgg
	kapbr11A11	gggTggcTggAgAcTgggTcATcTggATgTcTTgTgcAcTgTgAcAgAgg
20	kapbr11B3	gggAgTcTggAgAcTgggTcATcTggATgTcTTgTgcAcTgTgAcAgAgg
	Extender (5' biotinylated)	
kapext1bio		ccTcTgTcAcAgTgcAcAAgAcATccAgATgAccccAgTcTcc
Primers		
25	kaPCRt1	ccTcTgTcAcAgTgcAcAAgAc
	kapfor	5'-aca ctc tcc cct gtt gaa gct ctt-3'

30	Table 530
PCR program for amplification of kappa DNA	
95°C	5 minutes
95°C	15 seconds
65°C	30 seconds

72°C 1 minute
72°C 7 minutes
4°C hold

5 Reagents (100 ul reaction):

Template	50 ng
10x turbo PCR buffer	1x
turbo Pfu	4U
dNTPs	200 µM each
10 kaPCRt1	300 nM
kapfor	300 nM

Table 610: Stuffer used in VH

1 TCCGGAGCTT CAGATCTGTT TGCCTTTTGG TGGGGTGGTG CAGATCGCGT TACGGAGATC
 61 GACCGACTGC TTGAGCAAAA GCCACGCTTA ACTGCTGATC AGGCATGGGA TGTATTTCGC
 121 CAAACCAGTC GTCAGGATCT TAACCTGAGG CTTTTTTAC CTACTCTGCA AGCAGCGACA
 181 TCTGGTTTGA CACAGAGCGA TCCGCCGTCGT CAGTTGGTAG AAACATTAAAC ACGTTGGGAT
 241 GGCATCAATT TGCTTAATGA TGATGGTAAA ACCTGGCAGC AGCCAGGCTC TGCCATCCTG
 301 AACGTTTGGC TGACCAAGTAT GTTGAAGCGT ACCGTAGTGG CTGCCGTACC TATGCCATT
 361 GATAAGTGGT ACAGCGCCAG TGGCTACGAA ACAACCCAGG ACGGCCAAC TGGTTCGCTG
 421 AATATAAGTG TTGGAGCAAA AATTTGTAT GAGCGGTGC AGGAGACAA ATCACCATT
 481 CCACAGGCGG TTGATCTGTT TGCTGGGAAA CCACAGCAGG AGTTGTGTT GGCTGCGCTG
 541 GAAGATACCT GGGAGACTCT TTCCAAACGC TATGGCAATA ATGTGAGTAA CTGGAAAACA
 601 CCTGCAATGG CCTTAACGTT CCGGGCAAT AATTCTTTG GTGTACCGCA GGCCGCAGCG
 661 GAAGAAACGC GTCATCAGGC GGAGTATCAA AACCGTGGAA CAGAAAACGA TATGATTGTT
 721 TTCTCACCAA CGACAAGCGA TCGTCCTGTG CTTGCCTGGG ATGTGGTCGC ACCCGTCA
 781 AGTGGGTTTA TTGCTCCCGA TGGAACAGTT GATAAGCACT ATGAAGATCA GCTGAAAATG
 841 TACGAAAATT TTGGCCGTAA GTCGCTCTGG TTAACGAAGC AGGATGTGGA GCGGCATAAG
 901 GAGTCGTCTA GA

Table 620: DNA sequence of pCES5
 ! pCES5 6680 bases = pCes4 with stuffers in CDR1-2 and CDR3 2000.12.13

```

5  ! Ngene = 6680
  ! Useful REs (cut MANoLI fewer than 3 times) 2000.06.05
  !
  ! Non-cutters
  ! Acc65I Ggtacc      AfeI AGCgct      AvrII Cctagg
  ! BsaBI GATNnnnntc  BsiWI Cgtacg      BsmFI Nnnnnnnnnnnnnnnngtcccc
  ! BsrGI Tgtaca      BstAPI GCANNNNntgc BstBI Ttcgaa
  ! BstZ17I GTATac    BtrI CACgtg      Ecl136I GAGctc
  ! EcoRV GATatc      FseI GGCCGGcc     KpnI GGTACc
  ! MscI TGGcca       NruI TCGcga      NsiI ATGCAT
  ! PacI TTAATtaa     PmeI GTTTaaac     PmlI CACgtg
  ! PpuMI RGGwccy     PshAI GACNNnnngtc SacI GAGCTC
  ! SacII CCGGgg      SbfI CCTGCagg     SexAI Accwgt
  ! SgfI GCGATcg      SnaBI TACgta      SpeI Actagt
  ! SphI GCATgc       Sse8387I CTGCAGg  StuI AGGcct
  ! SmaI ATTaaat      XmaI Cccggg
  !
  ! cutters
  ! Enzymes that cut more than 3 times.
  ! AlwNI CAGNNNctg   5
  ! BsgI ctgcac       4
  ! BsrFI Rccggy       5
  ! EarI CTCTTCnnnn   4
  ! FaeI nNNNNNGCGGG  10
  !
  ! Enzymes that cut from 1 to 3 times.
  ! EcoO109I Rggnccy   3 7 2636 4208
  ! BssSI Ctcgtg       1 12
  ! "- Cagag           1 1703
  ! BspHI Tcatga       3 43 148 1156
  ! AatII GACGTC       1 65
  ! BciVI GTATCCNNNNN  2 140 1667
  ! Eco57I CTGAAG      1 301
  ! "- cttcag          2 1349
  ! AvaI Cycgrg        3 319 2347 6137
  ! BsiHKAI GWGCWc     3 401 2321 4245
  ! HgiAI GWGCWc       3 401 2321 4245
  ! BglI gcannnnntcg   1 461
  ! ScaI AGTact        1 505

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5	!PvuI CGATcg	3	616	3598	5926
	!EspI TGCgca	2	763	5946	
	!BglI GCCNNNNnggc	3	864	2771	5952
	!BpmI CTGGAG	1	898		
	!-"- ctccag	1	4413		
	!BsaI GGTCCTCnnnn	1	916		
	!AhdI GACNNNNngtc	1	983		
	!Eam1105I GACNNNNngtc	1	983		
10	!DrdI GACNNNNngtc	3	1768	6197	6579
	!SapI gaagagc	1	1998		
	!PvuII CAGctg	3	2054	3689	5896
	!PflMI CCANNNNNtgg	3	2233	3943	3991
	!HindIII Agcctt	1	2235		
15	!ApaLI Gtgcac	1	2321		
	!BspMI Nnnnnnnngcaggt	1	2328		
	!-"- ACCTGCNNNNn	2	3460		
	!PstI CTGCAG	1	2335		
	!AccI GTmkac	2	2341	2611	
	!HincII GYrac	2	2341	3730	
20	!Sali Gtcgac	1	2341		
	!TliI Ctcgag	1	2347		
	!XhoI Ctcgag	1	2347		
	!BsiI gtcttc	2	2383	4219	
	!BlpI Gctnagc	1	2580		
25	!EspI Gctnagc	1	2580		
	!SgrAI CRccggyg	1	2648		
	!AgeI Accggt	2	2649	4302	
	!AscI GGcgcgcc	1	2689		
	!BshII Gcgcgcc	1	2690		
30	!SfiI GCCNNNNnggcc	1	2770		
	!NaeI GCCggc	2	2776	6349	
	!NcoMIV Gccggc	2	2776	6349	
	!BtgI Ccrggg	3	2781	3553	5712
	!DsaI Ccrggg	3	2781	3553	5712
35	!NcoI Ccatgg	1	2781		
	!StyI Ccwwgg	3	2781	4205	4472
	!MfeI Caattg	1	2795		
	!BspEI Tccgga	1	2861		
	!BglII Agatct	1	2872		
40	!BclI Tgatac	1	2956		
	!Bsu36I Cctnagg	3	3004	4143	4373
	!XcmI CCANNNNNnnntgg	1	3215		
	!MluI Acgcgt	1	3527		


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!HpaI GTTaaC      1 3730
!XbaI Tctaga      1 3767
!
5  !AflII Cttaag      1 3811
   !BsmI NGcatC      1 3821
   !"- GAATGCN      1 4695
   !RsrII CGgwoCg      1 3827
   !NheI GctagC      1 4166
   !BstEII Ggtnacc      1 4182
10 !BsmBI CGTCTCnmmn      2 4188 6625
   !"- Nnnnnngagacg      1 6673
   !ApaI GGGCCc      1 4209
   !BanII GRGcYc      3 4209 4492 6319
   !BspI20I Gggccc      1 4209
   !PspOMI Gggccc      1 4209
15 !BserI Nnnnnnnnnctctc      1 4226
   !"- GAGGAGNNNNNNNNNN      1 4957
   !EcoNI CCTNnnnagg      1 4278
   !PflPI GACNnngtc      1 4308
20 !TthI11I GACNnngtc      1 4308
   !KasI GgcgcC      2 4327 5967
   !BstXI CCANNNNNntgg      1 4415
   !NotI GCggccgc      1 4507
   !EagI Cggccg      1 4508
25 !BamHI Ggatcc      1 5169
   !BspDI ATcgat      1 5476
   !NdeI CATatg      1 5672
   !EcoRI Gaattc      1 5806
   !PstI TTATAa      1 6118
30 !DraIII CACNNNgtg      1 6243
   !BsaAI YACgtr      1 6246
!-----
! 1 gacgaaaagg cCTCGTGata cgcctatttt tataggttaa tgcacatgata ataattggttt
   BssSI.(1/2)
! 61 cttaGACGTC aggtggcact tttcggggaa atgtgcgcgg aaccctatt tgttatttt
   AatII.
! 121 tctaaataca ttcaaatatG TATCCgctca tgagacaata accctgataa atgcttcaat
   BciVI..(1 of 2)
! 181 aatattgaaa aaggaagagt
! Base # 201 to 1061 = Apr gene from pUC119 with some RE sites removed
!
! 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15
! fm S I Q H F R V A L I P F A

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201 atg agt att caa cat ttc cgt gtc gcc ctt att ccc ttt ttt gcg
 !
 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30
 A F C L P V F A H P E T L V K
 5 gca ttt tgc ctt cct gtt ttt gct cac cca gaa acg ctg gtg aaa
 !
 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45
 V K D A E D Q L G A R V G Y I
 10 gta aaa gat gct gaa gat cag ttg ggt gcc cga gtg ggt tac atc
 !
 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60
 E L D L N S G K I L E S F R P
 15 gaa ctg gat ctc aac agc ggt aag atc ctt gag agt ttt cgc ccc
 !
 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75
 E E R F P M M S T F K V L L C
 20 gaa gaa cgt ttt cca atg atg agc act ttt aaa gtt ctg cta tgt
 !
 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90
 G A V L S R I D A G Q E Q L G
 25 ggc gcg gta tta tcc cgt att gac gcc ggg caa gag CAa ctc ggt
 !
 91 92 93 94 95 96 97 98 99 100 101 102 103 104 105
 R R I H Y S Q N D L V E Y S P
 30 CGc cgc ata cac tat tct cag aat gac ttg gtt gAg TAc Tca cca
 !
 106 107 108 109 110 111 112 113 114 115 116 117 118 119 120
 V T E K H L T D G M T V R E L
 35 gtc aca gaa aag cat ctt acg gat gcc atg aca gta aga gaa tta
 !
 121 122 123 124 125 126 127 128 129 130 131 132 133 134 135
 C S A A I T M S D N T A A N L
 40 tgc agt gct gcc ata acc atg agt gat aac act gcg gcc aac tta
 !
 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150
 L L T T I G G P K E L T A F L
 45 ctt ctg aca aCG ATC Gga gga ccg aag gag cta acc gct ttt ttg
 !
 151 152 153 154 155 156 157 158 159 160 161 162 163 164 165
 H N M G D H V T R L D R W E P
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 166 167 168 169 170 171 172 173 174 175 176 177 178 179 180
 PvuI.... (1/2)
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 181 182 183 184 185 186 187 188 189 190 191 192 193 194 195
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651 cac aac atg ggg gat cat gta act cgc ctt gat cgt tgg gaa ccg
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 E L N E A I P N D E R D T T M
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 P V A M A T T L R K L L T G E
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 A D K V A G P L L R S A L P A
 831 gcg gat aaa gtt gca gga cca ctt ctg cgc tgc gcc ctt ccg gct
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 G W F I A D K S G A G E R G S
 876 ggc tgg ttt att gct gat aaa tCT GGA gcc ggt gag cgt gGG TCT
 BpmI..... (1/2) BsaI....
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 BsaI..... BsrDI.... (2/2)
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 I V V I Y T T G S Q A T M D E
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 Ahdi.....
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 R N R Q I A E I G A S L I K H
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 1081 catatatact ttagattgat ttaaaacttc atttttaatt taaaaggatc taggtgaaga
 ctgtcagac caagtttact

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! Vlight domains could be cloned in as ApaLI-XhoI fragments.
! VL-CL(kappa) segments can be cloned in as ApaLI-AscI fragments. <-----
5  |-----Ckappa-----
   | 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45
   | R  G  T  V  A  A  P  S  V  F  I  F  P  P  S
2359 | cgt gga act gtg gct gca cca tct GTC TTC atc ttc ccg cca tct
   |                                     BbsI...(1/2)
10 | 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60
   | D  E  Q  L  K  S  G  T  A  S  V  V  C  L  L
2404 | gat gag cag ttg aaa tct gga act gcc tct gtt gtg tgc ctg ctg
   |
15 | 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75
   | N  N  F  Y  P  R  E  A  K  V  Q  W  K  V  D
2449 | aat aac ttc tat ccc aga gag gcc aaa gta cag tgg aag gtg gat
   |
20 | 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90
   | N  A  L  Q  S  G  N  S  Q  E  S  V  T  E  Q
2494 | aac gcc ctc caa tcg ggt aac tcc cag gag agt gtc aca gag cag
   |
25 | 91 92 93 94 95 96 97 98 99 100 101 102 103 104 105
   | D  S  K  D  S  T  Y  S  L  S  S  T  L  T  L
2539 | gac agc aag gac agc acc tac agc ctc agc agc acc ctg acg CTG
   |                                     EspI...
30 | 106 107 108 109 110 111 112 113 114 115 116 117 118 119 120
   | S  K  A  D  Y  E  K  H  K  V  Y  A  C  E  V
2584 | AGC aaa gca tac gag aaa cac aaa GTC TAC gcc tgc gaa gtc
   | ...EspI....                               AccI...(2/2)
35 | 121 122 123 124 125 126 127 128 129 130 131 132 133 134 135
   | T  H  Q  G  L  S  S  P  V  T  K  S  F  N  R
2629 | acc cat cag ggc ctg agt tCA CCG GTg aca aag agc ttc aac agg
   |                                     AgeI...(1/2)
40 | 136 137 138 139 140
   | G  E  C  .  .
2674 | gga gag tgt taa taa GG CGCGCCaatt
   |                               AscI.....
   |                               BssHII.

```

```

2701      ctatttcaag gagacagtca ta
|
| PelB::3-23(stuffed)::CH1::III fusion gene
|
5      1 2 3 4 5 6 7 8 9 10 11 12 13 14 15
      M K Y L L P T A A A G L L L L
2723  atg aaa tac cta ttg cct acg gca gcc gct gga ttg tta tta ctc
|-----|
10      16 17 18 19 20 21 22
      A A Q P A M A
2768  gcG GCC cag ccG GCC atg gcc
      Sfil.....
15      NgoMIV..(1/2)
      NcoI....
|
| FR1(DP47/V3-23)-----
20      23 24 25 26 27 28 29 30
      E V Q L L E S G
2789  gaa|gtt|CAA|TTG|tta|gag|tct|ggt|
      | MfeI |
|
|-----FR1-----
25      31 32 33 34 35 36 37 38 39 40 41 42 43 44 45
      G G L V Q P G G S L R L S C A
2813  |ggc|ggt|ctt|ggt|cag|cct|ggt|ggt|tct|tta|cgt|ctt|tct|tgc|gct|
|
|-----FR1-----
30      46 47 48
      A S G
2858  |gct|TCC|GGA|
      | BspEI |
|
| Stuffer for CDR1, FR2, and CDR2----->
35      There are no stop codons in this stuffer.
|
2867      gcttcAGATC Tgtttgcctt
      BglII..
2887  ttgtgtgggt ggtgcagatc gcgttacgga gatcgaccga ctgcttgagc aaaagccacg
2947  cttaactgct GATCAGgcgt gggatgttat tcgcaaac acc agtcgtcagg atcttaacct
      BclI...
3007  gaggcctttt ttacctactc tgcaagcagc gacatctggt ttgacacaga gcgatccgcg
3067  tcgtcagttg gtagaacat taacacgttg ggatggcatc aatttgctta atgatgatgg

```

3127 taaaacctgg cagcagccag gctctgccat cctgaacgtt tggctgacca gtatgttgaa
3187 gcgtaccgta gtggctgccg tacctatgcc Atttgataag TGGtacagcg ccagtggcta
! XcmI.....
3247 cgaacaacc caggacggcc caactgggtc gctgaatata agtgttggag caaaaatttt
3307 gtatgagcgg gtgcaggagg acaaatcacc aatccacag ggggttgatc tgtttgtggy
3367 gaaaccacag caggaggttg tgttggctgc gctggaagat acctgggaga ctctttccaa
3427 acgctatggc aataatgtga gtaactggaa aacacctgca atggccttaa cgttccgggc
3487 aaataatttc tttgtgtac cgcaggccgc agcgggaaga ACGGTcatc aggcggagta
! MluI..
3547 tcaaaacctg ggaacagaaa acgatatgat tgtttctca ccaacgacaa gcgatcgtcc
3607 tgtgcttccc tgggatgtgg tgcaccccg tcaagtggyg tttattgctc ccgatggaac
3667 agttgataag cactatgaag atcagctgaa aatgtacgaa aatttggcc gtaagtgcgt
! PvuII.
3727 ctgGTTAACg aagcaggatg tggaggcgca taaggagtcg
! HpaI..
! HincII(2/2)
-----FR3-----
4 5 6 7 8 9 10 11 12 13 14 15 16
93 94 95 96 97 98 99 100 101 102 103 104 105
S R D N S K N T L Y L Q M
3767 |TCT|AGA|gac|aac|tct|aag|aat|act|ctc|tac|ttg|cag|atg|
! | XbaI |
-----FR3----->|
17 18 19 20
106 107 108 109
N S L S l s i r s g
3806 |aac|agc|TTA|AG t ctg agc att CGG TCC G
! |AflII |
! RsrII..
q h s p t .
3834 gg caa cat tct cca aac tga ccagacga cacaacggc
3872 ttacgctaaa tcccgcccat gggatggtaa agagtgggcg tcttggctgg cctggactca
3932 tcagatgaag gccaaaaatt ggcaggagtg gacacagcag gcagcgaac aagcactgac
3992 catcaactgg tactatgctg atgtaaacgg caatatgggt tatgttcata ctggtgctta
4052 tccagatcgt caatcaggcc atgatccgg attaccggtt cctggtagcg gaaaatggga
4112 ctggaaaagg ctattgcctt ttgaaatgaa ccctaagggtg tataaccccc ag
4164 aa GCTAGC ctgcggcttc
! NheI..
G|GTC|ACC| gtc tca agc
4182 | BstEII |
!

PCT/US01/12454

!
 4588 T V E S C L A K P H T E N S F
 act gtt gaa agt tgt tta gca aaa cct cat aca gaa aat tca ttt
 !
 5
 !
 181 182 183 184 185 186 187 188 189 190 191 192 193 194 195
 T N V W K D D K T L D R Y A N
 act aac gtc tgg aaa gac gac aaa act tta gat cgt tac gct aac
 4633
 !
 196 197 198 199 200 201 202 203 204 205 206 207 208 209 210
 Y E G C L W N A T G V V C T
 tat gag ggc tgt ctg tgg AAT GCT aca ggc gtt gtg gtt tgt act
 4678
 !
 BsmI....
 211 212 213 214 215 216 217 218 219 220 221 222 223 224 225
 G D E T Q C Y G T W V P I G L
 ggt gac gaa act cag tgt tac ggt aca tgg gtt cct att ggg ctt
 4723
 !
 226 227 228 229 230 231 232 233 234 235 236 237 238 239 240
 A I P E N E G G G S E G G S
 gct atc cct gaa aat gag ggt ggc tct gag ggt ggc ggt tct
 4768
 !
 241 242 243 244 245 246 247 248 249 250 251 252 253 254 255
 E G G S E G G T K P P E Y
 gag ggt ggc ggt tct gag ggt ggc ggt act aaa cct cct gag tac
 4813
 !
 256 257 258 259 260 261 262 263 264 265 266 267 268 269 270
 G D T P I P G Y T Y I N P L D
 ggt gat aca cct att ccg ggc tat act tat atc aac cct ctc gac
 4858
 !
 271 272 273 274 275 276 277 278 279 280 281 282 283 284 285
 G T Y P P G T E Q N P A N P N
 ggc act tat ccg cct ggt act gag caa aac ccc gct aat cct aat
 4903
 !
 286 287 288 289 290 291 292 293 294 295 296 297 298 299 300
 P S L E E S Q P L N T F M F Q
 cct tct ctt GAG GAG tct cag cct ctt aat act ttc atg ttt cag
 4948
 !
 BseRI..(2/2)
 301 302 303 304 305 306 307 308 309 310 311 312 313 314 315
 N N R F R N R Q G A L T V Y T
 aat aat agg ttc cga aat agg cag ggt gca tta act gtt tat acg
 4993
 !
 316 317 318 319 320 321 322 323 324 325 326 327 328 329 330
 G T V T Q G T D P V K T Y Y Q
 !
 40

5038 ggc act gtt act caa ggc act gac ccc gtt aaa act tat tac cag
 !
 !
 !
 5 Y T P V S S K A M Y D A Y W N
 5083 tac act cct gta tca tca aaa gcc atg tat gac gct tac tgg aac
 !
 !
 !
 346 347 348 349 350 351 352 353 354 355 356 357 358 359 360
 ! G K F R D C A F H S G F N E D
 5128 ggt aaa ttc aga gac tgc gct ttc cat tct ggc ttt aat gaG GAT
 ! BamHI...
 !
 !
 361 362 363 364 365 366 367 368 369 370 371 372 373 374 375
 ! P F V C E Y Q G S S D L P Q
 5173 CCa ttc gtt tgt gaa tat caa ggc caa tcg tct gAC CTG Cct caa
 ! BamHI... BspMI...(2/2)
 !
 !
 376 377 378 379 380 381 382 383 384 385 386 387 388 389 390
 ! P P V N A G G G S G G S G G
 5218 cct cct gtc aat gct ggc ggc ggc tct ggt ggt tct ggt ggc
 !
 !
 391 392 393 394 395 396 397 398 399 400 401 402 403 404 405
 ! G S E G G G S E G G G S E G G
 5263 ggc tct gag ggt ggc ggc tct gag ggt ggc ggt tct gag ggt ggc
 !
 !
 406 407 408 409 410 411 412 413 414 415 416 417 418 419 420
 ! G S E G G G S G G S G S G D
 5308 ggc tct gag ggt ggc ggt tcc ggt ggc ggc tcc ggt tcc ggt gat
 !
 !
 421 422 423 424 425 426 427 428 429 430 431 432 433 434 435
 ! F D Y E K M A N A N K G A M T
 5353 ttt gat tat gaa aaa atg gca aac gct aat aag ggg gct atg acc
 !
 !
 436 437 438 439 440 441 442 443 444 445 446 447 448 449 450
 ! E N A D E N A L Q S D A K G K
 5398 gaa aat gcc gat gaa aac gcg cta cag tct gac gct aaa ggc aaa
 !
 !
 451 452 453 454 455 456 457 458 459 460 461 462 463 464 465
 ! L D S V A T D Y G A A I D G F
 5443 ctt gat tct gtc gct act gat tac ggt gct gct ATC GAT ggt ttc
 ! BspDI...
 !
 !
 466 467 468 469 470 471 472 473 474 475 476 477 478 479 480
 ! I G D V S G L A N G N G A T G

```

5488 att ggt gac gtt tcc ggc ctt gct aat ggt aat ggt gct act ggt
!
!
!
5      481 482 483 484 485 486 487 488 489 490 491 492 493 494 495
!      D F A G S N S Q M A Q V G D G
!      5533 gat ttt gct ggc tct aat tcc caa atg gct caa gtc ggt gac ggt
!
!
!      496 497 498 499 500 501 502 503 504 505 506 507 508 509 510
!      D N S P L M N N F R Q Y L P S
!      5578 gat aat tca cct tta atg aat aat ttc cgt caa tat tta cct tct
!
!
!      511 512 513 514 515 516 517 518 519 520 521 522 523 524 525
!      L P Q S V E C R P Y V F G A G
!      5623 ttg cct cag tcg gtt gaa tgt cgc cct tat gtc ttt ggc gct ggt
!
!
!      526 527 528 529 530 531 532 533 534 535 536 537 538 539 540
!      K P Y E F S I D C D K I N L F
!      5668 aaa CCA TAT Gaa ttt tct att gat tgt gac aaa ata aac tta ttc
!      NdeI....
!
!
!      541 542 543 544 545 546 547 548 549 550 551 552 553 554 555
!      R G V F A F L L Y V A T F M Y
!      5713 cgt ggt gtc ttt gcg ttt ctt tta tat gtt gcc acc ttt atg tat
!
!
!      556 557 558 559 560 561 562 563 564 565 566 567 568 569 570
!      V F S T F A N I L R N K E S .
!      5758 gta ttt tcg acg ttt gct aac ata ctg cgt aat aag gag tct taa
!
!
!      571
!
!
!      5803 taa GAATTC
!      EcoRI.
!      5812 actggcgt cgttttacaa cgtcgtgact gggaacc c tggcgttacc caacttaac
!      5871 gccttgacg acatccccc ttcgccagct ggcgtaatag cgaagaggcc cgcacCGATC
!      PvuI...
!      5931 Gcccttccca acagtGCGC Agcctgaatg gcgaatGCGC Cctgatgcgg tattttctcc
!      ...PvuI... (3/3) FspI... (2/2) Kasi... (2/2)
!      5991 ttacgcattc gtgcgttatt tcacaccgca tataaatgtt aaacgttaat attttgttaa
!      6051 aattcgcgtt aaatttttgt taaatcagct cattttttaa ccaataggcc gaaatcgcca
!      6111 aaatccctTA TAAatcaaaa gaatagcccg agatagggtt gagtgttgtt ccagtttgga
!      PsiI...
!      6171 acaagagtc actattaaag aacgtggact ccaacgtcaa agggcgaaaa accgtctatc
!      6231 agggcgatgg ccCActacGT Gaaccatcac ccaaatcaag tttttgggg tcgaggtgcc
!      DraIII....

```

6291 gtaagcact aaatcggaac cctaaaggga gcccccgatt tagagcttga cggggaaaGC
! CCGCGaacgt ggcgagaaaag gaagggaaga aagcgaaagy agcgggcgct agggcgctgg
! 6351 --.NgomIV. (2/2) NgoMIV..
6411 caagtgtagc ggtcacgctg cgcgtaacca ccacaccgc cgcgttaat gcgccgctac
6471 agggcgcgta ctatggttgc tttagcgggt gcagtctcag tacaatctgc tctgatgccg
6531 catagttaag ccagccccga caccgcgcaa caccgctga cgcgccctga cgggcttgc
6591 tgctccggc atccgcttac agacaagctg tgaccgtctc cgggagctgc atgtgtcaga
6651 gggtttcacc gtcataccg aaacgcgcga

Table 630: Oligonucleotides used to clone CDR1/2 diversity

All sequences are 5' to 3'.

5	1) ON_CD1Bsp, 30 bases	
	A C C T C A C T g g C T T C C g g A	
	1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18	
10	T T C A C T T T C T C T	
	19 20 21 22 23 24 25 26 27 28 29 30	
	2) ON_Br12, 42 bases	
15	A g A A A C C C A C T C C A A A C C	
	1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18	
	T T T A C C A g g A g C T T g g C g	
	19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36	
20	A A C C C A	
	37 38 39 40 41 42	
	3) ON_CD2Xba, 51 bases	
25	g g A A g g C A g T g A T C T A g A	
	1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18	
	g A T A g T g A A g C g A C C T T T	
30	19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36	
	A A C g g A g T C A g C A T A	
	37 38 39 40 41 42 43 44 45 46 47 48 49 50 51	
35	4) ON_BotXba, 23 bases	

g	g	A	A	A	g	g	g	c	A	g	T	g	A	T	c	T	A	g	A
1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18		
5	19	20	21	22	23														

10 End Tables